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Run on: February 20, 2003, 16:27:07 ; Search time 33.600000
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(without alignments)
654.139 Million cell updates/sec

Title: US-09-855-313A-2
Perfect score: 835
Sequence: 1 MRISKPHLRISIOCYCLT...
NTKEEDCEWTHVWVWV... 1

Scoring table: BLOSUM62

Searched: 908470 seqs, 133250620 residues

... .. satisfying chosen parameters: 908470

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_101002:*

1: *SIDS2/gcgdata/geneseq/genescp-emb1/AA1980.DAT **
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8: *SIDS2/gcgdata/geneseq/genescp-emb1/AA1987.DAT **
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12: *SIDS2/gcgdata/geneseq/genescp-emb1/AA1991.DAT **
13: *SIDS2/gcgdata/geneseq/genescp-emb1/AA1992.DAT **
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18: *SIDS2/gcgdata/geneseq/genescp-emb1/AA1997.DAT **
19: *SIDS2/gcgdata/geneseq/genescp-emb1/AA1998.DAT **
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21: *SIDS2/gcgdata/geneseq/genescp-emb1/AA2000.DAT **
22: *SIDS2/gcgdata/geneseq/genescp-emb1/AA2001.DAT **
23: *SIDS2/gcgdata/geneseq/genescp-emb1/AA2002.DAT **

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	835	100.0	162	18	AAW37370	Mutant Interleukin
2	835	100.0	162	23	AAU77994	Human IL-15 double
3	835	100.0	162	23	ABR08335	Human interleukin
4	829	99.3	162	23	AAU77996	Human IL-15 single
5	829	99.3	162	23	AAU77997	Human IL-15 single
6	823	98.6	162	16	AAH83438	Human interleukin
7	823	98.6	162	16	AAH66927	Human IL-15. Homo
8	823	98.6	162	17	AAW09098	Simian epithelium
9	823	98.6	162	17	AAW07255	Human epithelium
10	823	98.6	162	17	AAH98527	Human interleukin

11	823	98.6	162	18	AAM37366	Wild-type interleukin-11
12	823	98.6	162	18	AAW01658	Human interleukin-12
13	823	98.6	162	19	AAW58187	Human interleukin-13
14	823	98.6	162	19	AAW31855	Human interleukin-14
15	823	98.6	162	20	AAV03756	Simian epithelium
16	823	98.6	162	21	AAH18632	Simian epithelium
17	823	98.6	162	21	AAV78595	Amino acid sequence
18	823	98.6	162	21	AAV52308	Human interleukin-16
19	823	98.6	162	22	AAE08576	Simian epithelium
20	823	98.6	162	22	AAE65202	Human interleukin-17
21	823	98.6	162	22	AAE66397	Simian EPF (SEPF)
22	823	98.6	162	22	AAE50870	Human interleukin-18
23	823	98.6	162	23	AAE08130	Human IL-15. Homo
24	823	98.6	162	23	AAU77995	Human interleukin-19
25	823	98.6	162	23	AAU07995	Human IL-16-type II
26	823	98.6	162	23	AAE08336	Mutant human inter
27	823	98.6	162	23	AAO14116	Human IL-15 polype
28	795	95.2	162	16	AAAR3436	Simian interleukin-1
29	795	95.2	162	16	AAE69265	Simian IL-15. Cer
30	795	95.2	162	17	AAAO9100	Human interleukin-2
31	795	95.2	162	17	AAAO7254	Simian epithelium d
32	795	95.2	162	17	AAE98556	Simian epithelium d
33	795	95.2	162	17	AAE92758	Simian interleukin
34	795	95.2	162	19	AAE39187	Mammalian interlea
35	795	95.2	162	20	AAV03758	Human epithelium d
36	795	95.2	162	21	AAV78594	Human epithelium d
37	795	95.2	162	21	AAV52310	Simian interleukin
38	795	95.2	162	22	AAE65962	Human epithelium d
39	627	75.2	162	22	AAE65962	Human EPF (bEPF) p
40	571	68.4	135	21	AAV54825	Simian interleukin-4
41	571	68.4	114	16	AAAR3310	Human interleukin-5
42	571	68.4	114	16	AAAO9099	Human interleukin-6
43	571	68.4	114	17	AAW39186	Simian mature epit
44	571	68.4	114	20	AAV03757	Simian epithelium
45	571	68.4	114	21	AAV52309	Simian epithelium

ALIGNMENTS

```

RESULT 1
AAW37370
ID      AAW37370 standard; Protein; 162 AA.
XX

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AC AAW37370,
XX

07-MAY-1998 (first entry)
XX

XX
XX
XXXXXXX-15 (15-15)

XX psoriasis; multiple sclerosis; type 1 diabetes; AIDS.

05 Homo sapiens
05 Synthetic.

FT	key Peptide	Location/Qualifiers
1	48	

peptide 1.1.48

Protein	/note="signal sequ
FT	49-162

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/NOTE="mature prot

```

misc-difference 149

F ¹	Misc-difference	/noce-wild-type G
	156.0	

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/note= "wild-type G
XX
E9T

```

PN W09741232-A7

XX XX

06-NOV-1997. PD XX

PF 25-APR-1997; 97WO-11506931

XX 26-APR-1996: 96US-0016634.
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA Maslinski W, Strom T;
 PI WPI: 1997-549734/50.
 DR N-PSDB; AAT97228.
 XX
 PT Mutant interleukin 15 polypeptide(s) - used for treating auto-immune
 diseases e.g. psoriasis, multiple sclerosis etc.
 XX
 PS Disclosure; Page 57; 86pp; English.
 XX
 CC This is the mutant interleukin-15 (IL-15) polypeptide. The wild-type
 CC IL-15 sequence can be mutated at codon positions 149 and 156 to create
 CC this mutant IL-15 polypeptide. This mutant polypeptide is at least 90%
 CC identical to the wild-type IL-15 and is capable of inhibiting at least
 CC one of the cellular events that normally occurs when the wild-type IL-15
 CC specifically binds to a cell surface receptor. The mutant IL-15 is used
 CC for suppressing the immune response in a patient. It can be used for
 CC treating autoimmune diseases such as rheumatic arthritis, type I diabetes
 CC or a rheumatic disease selected from systemic lupus erythematosus (SLE),
 CC Sjogren's syndrome, scleroderma, mixed connective tissue disease,
 CC dermatomyositis, polymyositis, Reiter's syndrome and Behcet's disease.
 CC It can also be used to treat Hashimoto's thyroiditis, Grave's disease,
 CC multiple sclerosis, myasthenia gravis, encephalomyelitis, a variety of
 CC pemphigus, psoriasis, inflammatory bowel disease, AIDS and vascular
 CC injury. The mutant IL-15 can also be used for reducing the viability of
 CC a cell that expresses a IL-15 receptor. It can also be used to diagnose
 CC a disease treatable with an IL-15 antagonist.
 XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 835; DB 18; Length 162;
 Best Local Similarity 100.0%; Pred. No. 6, 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRISKPHLRISISIOCYCLILNSHFTLGTAGIHVFLTGCSAGLPKTEANWVVISDLKKI 60
 DB 1 MRISKPHLRISISIOCYCLILNSHFTLGTAGIHVFLTGCSAGLPKTEANWVVISDLKKI 60
 QY 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVVISLSDGASHDVTENLILIAN 120
 DB 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVVISLSDGASHDVTENLILIAN 120
 QY 121 SLSSNGVNTSGCKCELEKRNKEFLDSFVHYIDMFINTS 162
 DB 121 SLSSNGVNTSGCKCELEKRNKEFLDSFVHYIDMFINTS 162
 DE Human IL-15 double mutant (Q149D and Q156D).
 XX
 XX Human; Interleukin-15 receptor; IL-15R; Interleukin-2 receptor; IL-2R;
 XX immune response; autoimmune disease; Rheumatoid arthritis; psoriasis;
 XX Reiter's syndrome; type I diabetes; Graves' disease; multiple sclerosis;
 XX inflammatory bowel disease; acquired immune deficiency syndrome; AIDS;
 XX transplantation; graft versus host disease; T-cell death; ADCC;
 XX activation induced cell death; passive cell death; ADCC; CDC;
 XX antibody dependent cell-mediated cytotoxicity; mutant; mutein;
 XX complement directed cytotoxicity.
 XX
 XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..48
 FT /label= Signal-peptide
 FT /label= 49..162
 FT Protein /label= Mature_IL-15_double_mutant
 FT Misc-difference 149 /note= "Substitution of wild type Gln to Asp"
 FT /note= "Substitution of wild type Gln to Asp"
 FT Misc-difference 156 /note= "Substitution of wild type Gln to Asp"
 XX
 PN W020022805-A2.
 PD 21-MAR-2002.
 XX
 PF 14-SEP-2001: 2001W0-US28612.
 XX
 PR 14-SEP-2000: 2000US-232251P.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PI Li XC, Strom T, Zheng XX;
 XX
 XX WPI: 2002-329953/36.
 DR N-PSDB; ABK47773.
 XX
 PT Therapeutic compositions comprising a first agent that targets an
 PT interleukin-15 receptor (IL-15R) and a second agent that targets an
 PT interleukin-2 receptor (IL-2R).
 XX
 PS Claim 8; Fig 1; 80pp; English.
 CC The present invention relates to a therapeutic composition comprising
 CC a first agent that targets an interleukin-15 receptor (IL-15R) and a
 CC second agent that targets an interleukin-2 receptor (IL-2R). The
 CC therapeutic composition is useful for suppressing an immune response
 CC in a patient where the patient has or is at risk of developing an immune
 CC disease, particularly an autoimmune disease such as rheumatoid arthritis,
 CC Reiter's syndrome and Behcet's disease, type I diabetes, Graves' disease,
 CC multiple sclerosis, pemphigus vulgaris, psoriasis, inflammatory bowel
 CC disease, and acquired immune deficiency syndrome (AIDS). It is also
 CC useful in patients having received a transplant organ, tissue or cell,
 CC and in patients having graft versus host disease. The pharmaceutical
 CC compositions are useful for promoting T-cell death which includes ADCC
 CC (activation induced cell death), passive cell death, ADCC (antibody
 CC dependent cell mediated cytotoxicity) or CDC (complement directed
 CC cytotoxicity). The present sequence representing human IL-15 double
 CC mutant (Q149D and Q156D) can be used in a therapeutic composition
 CC of the invention.
 CC Note: The present sequence referred to as Seq ID No 4 (mutant) on
 CC page 6 is shown as Seq ID No 2 in Fig 1.
 XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 835; DB 23; Length 162;
 Best Local Similarity 100.0%; Pred. No. 6, 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRISKPHLRISISIOCYCLILNSHFTLGTAGIHVFLTGCSAGLPKTEANWVVISDLKKI 60
 DB 1 MRISKPHLRISISIOCYCLILNSHFTLGTAGIHVFLTGCSAGLPKTEANWVVISDLKKI 60
 QY 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVVISLSDGASHDVTENLILIAN 120
 DB 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVVISLSDGASHDVTENLILIAN 120
 QY 121 SLSSNGVNTSGCKCELEKRNKEFLDSFVHYIDMFINTS 162
 DB 121 SLSSNGVNTSGCKCELEKRNKEFLDSFVHYIDMFINTS 162
 DE Human IL-15 double mutant (Q149D and Q156D).
 XX
 XX Human; Interleukin-15 receptor; IL-15R; Interleukin-2 receptor; IL-2R;
 XX immune response; autoimmune disease; Rheumatoid arthritis; psoriasis;
 XX Reiter's syndrome; type I diabetes; Graves' disease; multiple sclerosis;
 XX inflammatory bowel disease; acquired immune deficiency syndrome; AIDS;
 XX transplantation; graft versus host disease; T-cell death; ADCC;
 XX activation induced cell death; passive cell death; ADCC; CDC;
 XX antibody dependent cell-mediated cytotoxicity; mutant; mutein;
 XX complement directed cytotoxicity.
 XX
 XX Homo sapiens.
 OS Synthetic.

ID ABB08335 standard; protein; 162 AA.
 AC ABB08335;
 DT 18-JUN-2002 (first entry)
 DE Human interleukin-15.
 KW Antiinflammatory; uropathic; antiinflammatory; dermatological; antidiabetic;
 KW immunosuppressive; anti-HIV; human immunodeficiency virus; antileukemic;
 KW antiproliferative; antithyroid; neuroprotective; vulnery; ophthalmological;
 KW vasotrophic; immune response suppression; autoimmune disease;
 KW systemic lupus erythematosus; rheumatoid arthritis; type I diabetes;
 KW type II diabetes; psoriasis; thyroid; gut; central nervous system;
 KW Hashimoto's thyroiditis; ulcerative colitis; Crohn's disease;
 KW multiple sclerosis; myasthenia gravis; AIDS; vascular injury;
 KW acquired immune deficiency syndrome; organ transplant; malignant cell;
 KW IL-15R; interleukin-15 receptor; IL15R; non-immunogenic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..48
 FT /label= Signal_peptide
 FT Protein 49..162
 FT /label= Mature_IL-15
 PN MO200187330-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15578.
 XX
 PR 12-MAY-2000; 2000US-203801P.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PI Strom TB, Maslinski W, Zheng XX, Kim YS, Laczaz SF;
 DR WPI: 2002-089831/12.
 DR N-PSDB; ABA02510.
 PT Composition for treating immune diseases, especially autoimmune
 PT diseases, has agent targeting interleukin-15 receptor and agent that
 PT inhibits costimulatory signal transmitted between T cell and
 PT antigen-presenting cell.
 PS
 PS Disclosure; Fig 1; 42pp; English.
 XX
 CC The present sequence is that of interleukin-15 (IL-15), a cytokine and T
 CC cell growth factor encoded by the nucleic acid given in ABA02510. The
 CC specification describes a therapeutic composition comprising an agent
 CC that targets an IL-15 receptor (IL-15R) and a second agent that inhibits
 CC a costimulatory signal transmitted between an antigen-presenting cell and
 CC a T cell. The composition of the invention has antileukemic, utopathic,
 CC antiinflammatory, dermatological, antidiabetic, immunosuppressive,
 CC anti-HIV (human immunodeficiency virus), antileukemic, antiproliferative,
 CC antithyroid, neuroprotective, vulnery, ophthalmological and vasotrophic
 CC activities. The inventive composition is useful for immune response
 CC suppression in patients having an immune disease, particularly an
 CC autoimmune disease. Diseases include rheumatic disease such as systemic
 CC lupus erythematosus, rheumatoid arthritis; type I or type II diabetes;
 CC psoriasis; autoimmune diseases of the thyroid, gut and central nervous
 CC system e.g. Hashimoto's thyroiditis, ulcerative colitis, Crohn's disease,
 CC multiple sclerosis and myasthenia gravis. The inventive agents may be
 CC used to treat acquired immune deficiency syndrome (AIDS) and for
 CC suppressing an immune response in patients who have received an organ,
 CC tissue or cell transplant or vascular injury. The agents may be used to
 CC eliminate malignant or immune system cells. The alpha subunit of IL-15R
 CC is expressed by activated or malignant immune cells, but not by resting
 CC immune cells, the agents specifically target those cells that have been
 CC activated or that have become malignant. Mutant IL-15 is not immunogenic
 CC and binds the IL-15Rapha with the same affinity as wild type IL-15.

XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 835; DB 23; Length 162;
 Best local similarity 100.0%; Pred. No. 6, 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRISKPHRSISIQCYLCILNSHTEAGIHVFLIGCSAGLFRKTNMWNYSDLKRI 60
 Db 1 MRISKPHRSISIQCYLCILNSHTEAGIHVFLIGCSAGLFRKTNMWNYSDLKRI 60
 QY 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELQVLSLESDASTHPTVENLIILANN 120
 Db 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELQVLSLESDASTHPTVENLIILANN 120
 QY 121 SLSSNGVWTEGCKECEELEKNIKEFLDSFYHIVDMFLNLS 162
 Db 121 SLSSNGVWTEGCKECEELEKNIKEFLDSFYHIVDMFLNLS 162

RESULT 4

AAU77996
 ID AAU77996 standard; Protein; 162 AA.
 XX
 AC AAU77996;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human IL-15 single mutant (Q149D).
 XX
 KW Human; interleukin-15 receptor; IL-15R; interleukin-2 receptor; IL-2R;
 KW immune response; autoimmune disease; rheumatoid arthritis; psoriasis;
 KW Kellier's syndrome; type I diabetes; Graves' disease; multiple sclerosis;
 KW inflammatory bowel disease; acquired immune deficiency syndrome; AIDS;
 KW transplantation; graft versus host disease; T-cell death; AIDS;
 KW activation induced cell death; passive cell death; AOCG; CDC;
 KW antibody dependent cell-mediated cytotoxicity; mutant; mutain;
 KW complement directed cytotoxicity.
 KW
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..48
 FH /label= Signal_peptide
 FH Protein 49..162
 FH /label= Mature_IL-15_single_mutant_(Q101D)
 FT Misc-difference 149 /note= "Substitution of wild type Glu to Asp"
 FT
 PN MO200222805-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 14-SEP-2001; 2001WO-US28612.
 XX
 PR 14-SEP-2000; 2000US-232251P.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PI Li XC, Strom T, Zheng XX;
 DR WPI: 2002-329953/36.
 DR
 DR
 DR
 PT Therapeutic compositions comprising a first agent that targets an
 PT interleukin-15 receptor (IL-15R) and a second agent that targets an
 PT interleukin-2 receptor (IL-2R).
 PS Claim 7; Page -: 80pp; English.
 CC
 CC The present invention relates to a therapeutic composition comprising
 CC a first agent that targets an interleukin-15 receptor (IL-15R) and a
 CC second agent that targets an interleukin-2 receptor (IL-2R). The

PR 14-SEP-2000; 200005-232251P.
XX

06-APR-1994; 94WO-US03793.
PF

XX 06-APR-1994; 94WO-0503793.
 XX (IMMV) IMMUNEX CORP.
 XX
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX
 DR WPI: 1995-373556/48.
 DR N-PSDB: AAT00526.
 XX
 PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
 PT stimulates proliferation and differentiation of T cells, used for
 PT treating carcinoma(s), melanomas, etc. and viral infections
 XX
 PS Claim 24: Page 28-29; 48pp; English.

CC A simian species of IL-15 (sIL-15) was purified and its AA
 CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,
 CC AAT00524, AAT00525). Both the simian and the human ORFs encode
 CC a precursor polypeptide (AAR83436, AAR83438). The precursor
 CC encoding mature simian or human IL-15 polypeptides and a sequence
 CC simian and human IL-15 polypeptides are disclosed in AAR83309 &
 CC IL-15, including human IL-15, that hybridize to probes defined by
 CC AAR83438. A plasmid contg. a recombinant clone of human IL-15
 CC cDNA was deposited with ATCC on Feb. 19, 1993 under ATCC 69245.
 CC The deposit was named 141-herf. AAR83435 is a mammalian mature
 CC IL-15 polypeptide. It is a generic sequence which encompasses both
 CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
 XX
 SQ Sequence 162 AA:

Query Match
 Best Local Similarity 98.6%; Score 823; DB 16; Length 162;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRISKPHLRISISIOCYLCLLNSHFLTEAGIHVFTLGCFSAGLPKTEAMWVVISDLKRI 60
 DB 1 MRISKPHLRISISIOCYLCLLNSHFLTEAGIHVFTLGCFSAGLPKTEAMWVVISDLKRI 60
 QY 61 EDLIQSMHIDATLTYESDVHPSCVYAMKCFLELOVTSLESGDASHDTVENLITLANN 120
 DB 61 EDLIQSMHIDATLTYESDVHPSCVYAMKCFLELOVTSLESGDASHDTVENLITLANN 120
 QY 121 SLSSNGVNTESGCKCEPELEKNIKPEFLDSFVHYIDMFINTS 162
 DB 121 SLSSNGVNTESGCKCEPELEKNIKPEFLDSFVHYIDMFINTS 162

RESULT 7
 AAR66927
 ID AAR66927 standard; Protein: 162 AA.
 AC AAR66927;
 DT 04-SEP-1995 (first entry)
 XX
 DE Human IL-15.
 KW Interleukin-15; IL-15; hIL-15; T-cell growth factor;
 KW antitumor; virucide.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT 1..48 Location/Qualifiers
 FT /label= Sig-peptide
 FT 49..162
 FT /label= Mat-peptide
 FT /note= "active human IL-15"

PN ZA9402636-A.
 XX 28-DEC-1994.
 PD 28-DEC-1994.
 XX
 PF 18-APR-1994; 94ZA-0002636.
 XX
 PR 18-APR-1994; 94ZA-0002636.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX
 DR WPI: 1995-082473/11.
 DR N-PSDB: AA084584.
 XX
 PT New purified interleukin-15 - which induces T cell proliferation
 PT and differentiation, used for the treatment of tumours and viral
 PT infection
 XX
 PS Claim 24: Page 28-29; 47pp; English.

CC A sIL-15 probe was prepared from isolated simian interleukin-15
 CC cDNA and used to screen a cDNA library generated from the IMTH
 CC cell line derived from human bone marrow stromal cells. Clone
 CC 141-herf encoded human IL-15.
 XX
 SQ Sequence 162 AA:

Query Match
 Best Local Similarity 98.6%; Score 823; DB 16; Length 162;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRISKPHLRISISIOCYLCLLNSHFLTEAGIHVFTLGCFSAGLPKTEAMWVVISDLKRI 60
 DB 1 MRISKPHLRISISIOCYLCLLNSHFLTEAGIHVFTLGCFSAGLPKTEAMWVVISDLKRI 60
 QY 61 EDLIQSMHIDATLTYESDVHPSCVYAMKCFLELOVTSLESGDASHDTVENLITLANN 120
 DB 61 EDLIQSMHIDATLTYESDVHPSCVYAMKCFLELOVTSLESGDASHDTVENLITLANN 120
 QY 121 SLSSNGVNTESGCKCEPELEKNIKPEFLDSFVHYIDMFINTS 162
 DB 121 SLSSNGVNTESGCKCEPELEKNIKPEFLDSFVHYIDMFINTS 162

RESULT 8
 AAM09098
 ID AAM09098 standard; Protein: 162 AA.
 AC AAM09098;
 DT 11-MAR-1997 (first entry)
 XX
 DE Simian epithelium derived T cell factor precursor.
 KW sETf; African green monkey; CV1/EBNA cell; T-cell; B-cell;
 KW lymphocyte; proliferation; differentiation; gastrointestinal;
 KW HIV infection; human immunodeficiency virus.
 XX
 OS Cercopithecus aethiops.
 XX
 FH Key
 FT Peptide
 FT 1..48 Location/Qualifiers
 FT /label= leader
 FT 49..162
 FT /label= mature-setf

PN US574138-A.
 XX 12-NOV-1996.
 PD 12-NOV-1996.
 XX
 PF 08-MAR-1993; 93US-0031399.

XX 22-FEB-1995: 950S-0393305.
 PR 08-MAR-1993: 93US-0031399.
 PR 22-APR-1994: 94US-0233606.
 XX
 XX (IMMUNEX CORP.
 PA
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX
 XX WPI: 1996-517923/51.
 DR N-PSDB: AAT49455.
 XX
 PT New epithelium derived T cell factor - induces proliferation of T
 PT and B cells, stimulates destruction of tumor and virus-infected
 PT cells and protects against toxicity, partic. for treating intestinal
 PT disease and HIV infection
 XX
 PS Claim 1; Fig 1; 35pp; English.
 XX
 CC The simian ETF (epithelium derived T cell factor) was isolated from
 CC African green monkey CV1/EBNA cell conditioned medium. The N-
 CC terminal sequence of the purified SETP was determined and then PCR
 CC primers were designed based on the sequence information. A 92 bp
 CC fragment was amplified from CV1/EBNA DNA and was used as a probe to
 CC screen a CV1/EBNA cDNA library for the full-length SETP coding
 CC sequence. Mature SETP induces proliferation and/or differentiation
 CC of precursor or mature T cells and is useful for promoting long-term
 CC in vitro culture of T-lymphocytes and T-cell lines. It is used for
 CC treating gastrointestinal diseases including peptic ulcer, colitis and
 CC malignancy and for treating HIV infection.
 XX
 SQ Sequence 162 AA;
 Query Match 98.6%; Score 823; DB 17; Length 162;
 Best Local Similarity 98.8%; Pred. No. 1.4e-84;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 MRISKPHLRISISIOCYCLLLNSHFLTEAGIHVFLGCFSAGLPTEANWVNIISDLKTI 60
 DB 1 MRISKPHLRISISIOCYCLLLNSHFLTEAGIHVFLGCFSAGLPTEANWVNIISDLKTI 60
 OY 61 EDLQSMHIDATLTESDVHPSCKYAMKCFLELOVYISLESGDASIHDTVENIILANN 120
 DB 61 EDLQSMHIDATLTESDVHPSCKYAMKCFLELOVYISLESGDASIHDTVENIILANN 120
 OY 121 SLSSNGNVTESGCKECELLEKNIKRFLOSFVHIVQMFINTS 162
 DB 121 SLSSNGNVTESGCKECELLEKNIKRFLOSFVHIVQMFINTS 162
 RESULT 9
 AAM07255
 ID AAM07255 standard; Protein: 162 AA.
 XX
 XX AAM07255;
 AC
 XX
 XX 05-FEB-1997 (first entry)
 DT
 XX
 XX Human epithelium-derived T cell factor.
 DE
 XX
 XX Epithelium-derived T-cell factor; simian; human; culture; proliferation;
 KW epithelial cell; differentiation; T-lymphocyte; African green monkey;
 KW primer; PCR; polymerase chain reaction; amplification; probe.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1..48
 FT /note= "signal peptide"
 FT 49..162
 FT protein /note= "mature protein"
 FT
 XX

PN US5552303-A.
 XX
 PD 03-SEP-1996.
 XX
 XX 08-MAR-1993: 93US-0031399.
 PR
 XX 08-MAR-1993: 93US-0031399.
 PR
 XX (IMMUNEX CORP.
 PA
 PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
 PI Rauch C;
 XX
 XX WPI: 1996-412063/41.
 DR N-PSDB: AAT42243.
 XX
 PT New isolated simian and human epithelium-derived T-cell factors -
 PT which stimulate the proliferation and/or differentiation of
 PT T-lymphocytes and T-cell lines
 XX
 PS Claim 21; Column 23-24; 22pp; English.
 XX
 CC This is the amino acid sequence of a human epithelium-derived T-cell
 CC factor (ETF). The gene was obtained using a 1.37 kb fragment of the
 CC corresp. African green monkey gene (AAT42242) as a probe to screen a
 CC cDNA library constructed from RNA derived from the IMPLH cell line. This
 CC cell line is derived by stable transformation of a human bone marrow
 CC stromal cell culture with pSV3neo. From a pool of about 1000 cDNA
 CC clones, one clone 141 hETP contained the gene. ETP is a protein of 15-17
 CC kD which is expressed by epithelial cells and stimulates proliferation
 CC and/or differentiation of precursor and/or mature T cells. The protein
 CC is therefore useful for promoting long term in vivo culture of
 CC T-lymphocytes and T-cell lines.
 XX
 SQ Sequence 162 AA;
 Query Match 98.6%; Score 823; DB 17; Length 162;
 Best Local Similarity 98.8%; Pred. No. 1.4e-84;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 MRISKPHLRISISIOCYCLLLNSHFLTEAGIHVFLGCFSAGLPTEANWVNIISDLKTI 60
 DB 1 MRISKPHLRISISIOCYCLLLNSHFLTEAGIHVFLGCFSAGLPTEANWVNIISDLKTI 60
 OY 61 EDLQSMHIDATLTESDVHPSCKYAMKCFLELOVYISLESGDASIHDTVENIILANN 120
 DB 61 EDLQSMHIDATLTESDVHPSCKYAMKCFLELOVYISLESGDASIHDTVENIILANN 120
 OY 121 SLSSNGNVTESGCKECELLEKNIKRFLOSFVHIVQMFINTS 162
 DB 121 SLSSNGNVTESGCKECELLEKNIKRFLOSFVHIVQMFINTS 162
 RESULT 10
 AAR98527
 ID AAR98527 standard; Protein: 162 AA.
 XX
 XX AAR98527;
 AC
 XX
 XX 17-NOV-1996 (first entry)
 DT
 XX
 XX Human interleukin-15.
 DE
 XX
 XX Interleukin-15; antagonist; mutein; graft versus host disease;
 KW allograft; T-cell growth factor.
 KW
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 56
 FT /note= "preferred site for amino acid substn."
 FT 156
 FT Misc-difference /note= "preferred site for amino acid substn."
 FT
 XX

PN W09626274-A1.
 XX
 PD 29-AUG-1996.
 XX
 PF 21-FEB-1996; 96WO-0502520.
 XX
 PR 22-FEB-1995; 95US-0392317.
 XX
 PA (IMV) IMMUNEX CORP.
 XX
 PI Grabstein KH, Paxton RJ, Pettit DK;
 XX WPI: 1996-402367/40.
 DR N-PSDB; AAT973635.
 XX
 PT Antagonists of interleukin-15 - are used to treat patients having
 PT symptoms of graft-versus-host disease and for prolonging allo-graft
 PT survival
 XX
 PS Disclosure; Page 25; 32pp; English.
 XX
 CC Human interleukin-15 (IL-15) (AA098527) is a T-cell growth factor.
 CC Mutins of human IL-15 or simlan IL-15 (see also AA098526) are
 CC useful as antagonists of IL-15 and can be prep. by PCR-mediated
 CC mutagenesis of the encoding sequences (see also AAT96634-35).
 CC Preferred IL-15 mutants have amino acid substitutions at
 CC Asp56 and/or Glu156. Asp56 is believed to affect binding to the
 CC IL-15 receptor beta subunit, and Glu156 to affect binding to the
 CC residues with another amino acid (pret. setine or cysteine), signal
 CC transduction to cells is prevented while affinity for the IL-15
 CC receptor is maintained. The mutants are useful for treating
 CC graft-versus-host disease and for prolonging allograft survival.
 XX
 SO Sequence 162 AA;
 Query Match 98.6%; Score 823; DB 17; Length 162;
 Best Local Similarity 98.8%; Pred. No. 1.4e-84;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MRSKPHRLRSISIOCTCLLNLSHFLTEAGHVFILGCFSGAGLPKTEANWVVISDLKI 60
 DB 1 MRSKPHRLRSISIOCTCLLNLSHFLTEAGHVFILGCFSGAGLPKTEANWVVISDLKI 60
 QY 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVVISLESQDASHDVENLILANN 120
 DB 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVVISLESQDASHDVENLILANN 120
 QY 121 SLSSNGNVTESGCKECELFEKNIKEFLDSFVHIVDMFINTS 162
 DB 121 SLSSNGNVTESGCKECELFEKNIKEFLDSFVHIVDMFINTS 162
 RESULT 11
 ID AAW37369
 XX AAW37369 standard; Protein: 162 AA.
 AC AAW37369;
 XX
 DT 07-MAY-1998 (first entry)
 XX
 DE Wild-type interleukin-15 (IL-15).
 XX
 KW Interleukin-15, IL-15; mutant; human; treatment; autoimmune disease;
 KW psoriasis; multiple sclerosis; rheumatic arthritis; immune response;
 XX type 1 diabetes; AIDS.
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide 1.48
 FT /note= "signal sequence"
 FT Protein 49..162

FP /note= "mature IL-15 polypeptide"
 FT Misc-difference 149
 FT /note= "The specifications claims a substitution of
 FT Glu at this position to Asp"
 FT Misc-difference 156
 FT /note= "The specifications claims a substitution of
 FT Glu at this position to Asp"
 XX
 PN W09741232-A1.
 XX
 PD 06-NOV-1997.
 XX
 PF 25-APR-1997; 97WO-0506931.
 XX
 PR 26-APR-1996; 96US-0016634.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Maslinski W, Strom T;
 XX WPI: 1997-549734/50.
 DR N-PSDB; AAT97227.
 XX
 PT Mutant interleukin 15 polypeptide(s) - used for treating auto-immune
 PT diseases e.g psoriasis, multiple sclerosis etc.
 XX
 PS Claim 7; Pages 55-56; 86pp; English.
 XX
 CC This is the wild-type interleukin-15 (IL-15) polypeptide. This wild-type
 CC sequence can be mutated at codon positions 149 and 156 to create a mutant
 CC IL-15 polypeptide. The mutant polypeptide is at least 90% identical to
 CC the wild-type IL-15 and is capable of inhibiting at least one of the
 CC cellular events that normally occurs when the wild-type IL-15
 CC specifically binds to a cell surface receptor. The mutant IL-15
 CC for suppressing the immune response in a patient. It can be used for
 CC treating autoimmune diseases such as rheumatic arthritis, type 1 diabetes
 CC or a rheumatic disease selected from systemic lupus erythematosus (SLE),
 CC Sjogren's syndrome, scleroderma, mixed connective tissue disease,
 CC dermatomyositis, polymyositis, Reiter's syndrome and Behcet's disease.
 CC It can also be used to treat Hashimoto's thyroiditis, Grave's disease,
 CC multiple sclerosis, myasthenia gravis, encephalomyelitis, a variety of
 CC injuries. The mutant IL-15 can also be used for reducing the viability of
 CC a cell that expresses a IL-15 receptor. It can also be used to diagnose
 CC a disease treatable with an IL-15 antagonist.
 XX
 SO Sequence 162 AA;
 Query Match 98.6%; Score 823; DB 18; Length 162;
 Best Local Similarity 98.8%; Pred. No. 1.4e-84;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MRSKPHRLRSISIOCTCLLNLSHFLTEAGHVFILGCFSGAGLPKTEANWVVISDLKI 60
 DB 1 MRSKPHRLRSISIOCTCLLNLSHFLTEAGHVFILGCFSGAGLPKTEANWVVISDLKI 60
 QY 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVVISLESQDASHDVENLILANN 120
 DB 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVVISLESQDASHDVENLILANN 120
 QY 121 SLSSNGNVTESGCKECELFEKNIKEFLDSFVHIVDMFINTS 162
 DB 121 SLSSNGNVTESGCKECELFEKNIKEFLDSFVHIVDMFINTS 162
 RESULT 12
 ID AAW01658
 XX AAW01658 standard; Protein: 162 AA.
 AC AAW01658;
 XX
 DT 18-MAR-1997 (first entry)
 XX

DE Human interleukin-15.
 XX IL-15: interleukin-15; T-cell growth factor; proliferation; stimulate;
 KW muscle growth; differentiation; hypertrophy; treat; atrophy; wasting;
 KW skeletal; cardiac; muscle; congestive heart failure; diabetes-associated;
 KW glucose-intolerance; dyslipidaemia; rhabdomyosarcoma; dystrophy.
 XX Homo sapiens.
 XX OS
 XX PN MO9637223-A1.
 XX PD 28-NOV-1996.
 XX PF 07-MAY-1996: 96WO-US06423.
 XX PR 24-MAY-1995: 95US-0535733.
 XX PA (IMMUNEX) IMMUNEX CORP.
 XX PI Grabstein KH, Quinn LS, Trout AB;
 XX DR WPI: 1997-020939/02.
 XX N-PSDB: AAT58404.
 XX PT Muscle trophic compsn. contg. interleukin 15 - for treating, e.g.
 XX PT congestive heart failure, muscle wasting etc.
 XX PS Disclosure: Page 12: 22pp: English.
 XX CC This sequence is human interleukin-15 (IL-15), a known T-cell growth
 CC factor that can support proliferation of an IL-2-dependent cell line.
 CC CCIL-2. Compsn. contg. IL-15 to stimulate muscle growth, differentiation
 CC or hypertrophy are claimed. The stimulation of muscle growth is useful
 CC for treating atrophy, or wasting, in particular, skeletal and cardiac
 CC muscle atrophy. The compsn. further comprises a steroid, growth hormone
 CC and diabetes-associated glucose-intolerance or dyslipidaemia,
 CC CC rhabdomyosarcoma and muscular dystrophy can all be treated by such
 CC compsn..
 XX CC
 XX Sequence 162 AA:
 S0 Query Match 98.6%; Score 823; DB 18; Length 162;
 Best Local Similarity 98.8%; Pred. No. 1.4e-04;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MRISKPHLRISITQCYICLLNSHFLTEAGIHVFLIGCFSGAGLPKTEANWVVISDLKTI 60
 DB 1 MRISKPHLRISITQCYICLLNSHFLTEAGIHVFLIGCFSGAGLPKTEANWVVISDLKTI 60
 QY 61 EDLIQSMHIDATLTESDVHPSCKVTAMKCFLELQVLSLESGDASIHDTVENLILANN 120
 DB 61 EDLIQSMHIDATLTESDVHPSCKVTAMKCFLELQVLSLESGDASIHDTVENLILANN 120
 QY 121 SLSSNGNVTESGCKCELEFNKIKFELDSFVHIYDMFINTS 162
 DB 121 SLSSNGNVTESGCKCELEFNKIKFELDSFVHIYDMFINTS 162
 QY 121 SLSSNGNVTESGCKCELEFNKIKFELDSFVHIYDMFINTS 162
 DB 121 SLSSNGNVTESGCKCELEFNKIKFELDSFVHIYDMFINTS 162
 RESULT 13
 AAM53878
 ID AAM53878 standard: Protein: 162 AA.
 XX
 AC AAM53878:
 XX
 DT 13-JUL-1998 (first entry)
 XX
 DE Human interleukin-15.
 KW Human: interleukin-15; IL-15; T cell; B cell; proliferation; vaccine;
 KW cytokine; growth factor.
 XX
 XX Homo sapiens.
 OS

XX US5747024-A.
 XX PN
 XX PD 05-MAY-1998.
 XX PF 19-JUN-1995: 95US-0504042.
 XX PR 19-JUL-1995: 95US-0504042.
 XX PR 08-MAR-1993: 93US-0031399.
 XX PR 22-APR-1994: 94US-0233606.
 XX PR 22-FEB-1995: 95US-0393305.
 XX PA (IMMUNEX) IMMUNEX CORP.
 XX PI Grabstein KH, Widmer MB;
 XX DR WPI: 1998-285678/25.
 XX N-PSDB: AAY23554.
 XX PT Use of interleukin-15 - to enhance immunogenicity of a vaccine
 XX PS Disclosure: Column 5-6: 5pp: English.
 XX CC This sequence is human interleukin-15 (IL-15), which can be used in
 CC the vaccine of the invention. The vaccine composition comprises an
 CC immunogenic amount of a vaccine antigen (Ag) and an
 CC immunogenicity-augmenting amount of IL-15. The composition is useful for
 CC enhancing the immunogenicity of a vaccine. The cytokine IL-15 is a potent
 CC T and B cell growth factor. It causes proliferation and differentiation
 CC of these cells and augments T cell mediated immune responses. The vaccine
 CC composition can sufficiently elicit an immune response without being
 CC deleterious to the recipient, especially when using pathogenically
 CC deficient antigens. Some vaccines do not elicit a strong immune response
 CC and cannot provide sufficient protection on further exposure to the
 CC antigen.
 XX CC
 XX Sequence 162 AA:
 S0 Query Match 98.6%; Score 823; DB 19; Length 162;
 Best Local Similarity 98.8%; Pred. No. 1.4e-04;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MRISKPHLRISITQCYICLLNSHFLTEAGIHVFLIGCFSGAGLPKTEANWVVISDLKTI 60
 DB 1 MRISKPHLRISITQCYICLLNSHFLTEAGIHVFLIGCFSGAGLPKTEANWVVISDLKTI 60
 QY 61 EDLIQSMHIDATLTESDVHPSCKVTAMKCFLELQVLSLESGDASIHDTVENLILANN 120
 DB 61 EDLIQSMHIDATLTESDVHPSCKVTAMKCFLELQVLSLESGDASIHDTVENLILANN 120
 QY 121 SLSSNGNVTESGCKCELEFNKIKFELDSFVHIYDMFINTS 162
 DB 121 SLSSNGNVTESGCKCELEFNKIKFELDSFVHIYDMFINTS 162
 QY 121 SLSSNGNVTESGCKCELEFNKIKFELDSFVHIYDMFINTS 162
 DB 121 SLSSNGNVTESGCKCELEFNKIKFELDSFVHIYDMFINTS 162
 RESULT 14
 AAM39185
 ID AAM39185 standard: Protein: 162 AA.
 XX
 AC AAM39185:
 XX
 DT 08-MAY-1998 (first entry)
 XX
 DE Simian epithelium derived T-cell factor protein.
 KW Epithelium derived T-cell factor; ETP; simian; gastrointestinal disease;
 KW B-cell stimulation; epithelium; villi; CD4+; T-cell stimulation;
 KW treatment; prevention.
 XX
 XX Simian.
 OS
 XX Key Location/Qualifiers
 FT Peptide 1..48

FT Protein /Label= leader sequence
 FT 49..162
 XX /Label= ETF

US5707616-A.

13-JAN-1998.

04-OCT-1996;

96US-0726817.

22-FEB-1995;

95US-0393305.

08-MAR-1993;

93US-0031399.

22-APR-1994;

94US-0233606.

(IMMUNEX CORP.

Anderson DM, Eisenman JR, Fung V, Grabstein KH;

Rauch C;

WPI: 1998-100295/09.

N-PSDB: AAV02873.

PT Treatment or prevention of gastrointestinal diseases - by

administering epithelium-derived T-cell factor polypeptide

PS Disclosure: Column 35-38; 34pp: English.

XX This sequence represents a full length simian epithelium-derived T-cell
 CC factor (ETF) which is used in a method for treating or preventing
 CC gastrointestinal disease. These polypeptides have particular application
 CC in the treatment of gastrointestinal disorders associated with disruption
 CC of the gastrointestinal epithelium or villi such as chemotherapy- and
 CC radiation-induced enteritis (gut toxicity), mucositis, peptic
 CC ulcer disease, gastroenteritis and colitis, villus atrophic disorders,
 CC malignancy and inflammatory bowel disease. ETF polypeptides may also be
 CC useful in the treatment of human immunodeficiency virus (HIV) and
 CC HIV-associated disease due to their ability to stimulate CD4+ and CD8+
 CC cells. Biologically active ETF may be used to treat a variety of other
 CC diseases or conditions where T-cell or B cell stimulation is desired.

XX Sequence 162 AA:

Query Match 98.6%; Score 823; DB 19; Length 162;
 Best Local Similarity 98.8%; Pred. No. 1.4e-84;
 Matches 160: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MRISPHLRISISIOCYCLLNLSHFLTEAGIHVFLGCSAGLPKTEANWVVISDLKI 60

DB 1 MRISPHLRISISIOCYCLLNLSHFLTEAGIHVFLGCSAGLPKTEANWVVISDLKI 60

OY 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISLESQDASHDVEVLIILANN 120

DB 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISLESQDASHDVEVLIILANN 120

OY 121 SLSSNGVNTESGCKECEELEKNKEFLDSFVHIYDMFTNLS 162

DB 121 SLSSNGVNTESGCKECEELEKNKEFLDSFVHIYDMFTNLS 162

RESULT 15

AA03756

AA03756 standard: Protein, 162 AA.

AA03756:

10-UN-1999 (first entry)

Simian epithelium-derived T-cell factor (ETF) precursor polypeptide.

Epithelium-derived T-cell factor: ETF; immunoassay; enteritis; ulcer;

T cell proliferation; gastrointestinal disease; mucositis; colitis;

gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;

human immune deficiency virus; tumour; simian.

XX Mammalia.

XX US5892001-A.

XX 06-APR-1999.

XX 04-OCT-1996;

XX 96US-0725969.

XX 22-FEB-1995;

XX 95US-0393305.

XX 08-MAR-1993;

XX 93US-0031399.

XX 22-APR-1994;

XX 94US-0233606.

XX 04-OCT-1996;

XX 96US-0725969.

XX (IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX Rauch C;

XX WPI: 1999-253930/21.

XX N-PSDB: AAX29479.

XX Antibodies specific for epithelium-derived T-cell growth factor

XX Example 1; Columns 35-36; 34pp: English.

XX The invention relates to an isolated antibody that binds specifically to

XX a simian or human epithelium-derived T-cell factor (ETF) polypeptide. The

XX antibodies are used, optionally when immobilized or labeled, to detect

XX and quantify ETF in standard immunoassays. They may also be used as

XX their precursors or radiolabeled. ETF induces proliferation and/or

XX differentiation of T cells (or their precursors), e.g. for use in

XX establishing long term in vitro cultures; and is also used to treat

XX gastrointestinal disease (e.g. enteritis or mucositis induced by

XX chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis,

XX villus atrophy, malignancy and inflammatory bowel disease) to treat

XX human immune deficiency virus infection or associated disease, or

XX generally in any situation requiring stimulation of T or B cell

XX proliferation, secretion of immunoglobulins or certain cytokines.

XX increased anti-infectious disease immunity, induction of T-cell lytic

XX activity or increased destruction of tumour or virus-infected cells. The

XX present sequence represents a simian ETF precursor polypeptide sequence.

SO Sequence 162 AA:

Query Match 98.6%; Score 823; DB 20; Length 162;
 Best Local Similarity 98.8%; Pred. No. 1.4e-84;
 Matches 160: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MRISPHLRISISIOCYCLLNLSHFLTEAGIHVFLGCSAGLPKTEANWVVISDLKI 60

DB 1 MRISPHLRISISIOCYCLLNLSHFLTEAGIHVFLGCSAGLPKTEANWVVISDLKI 60

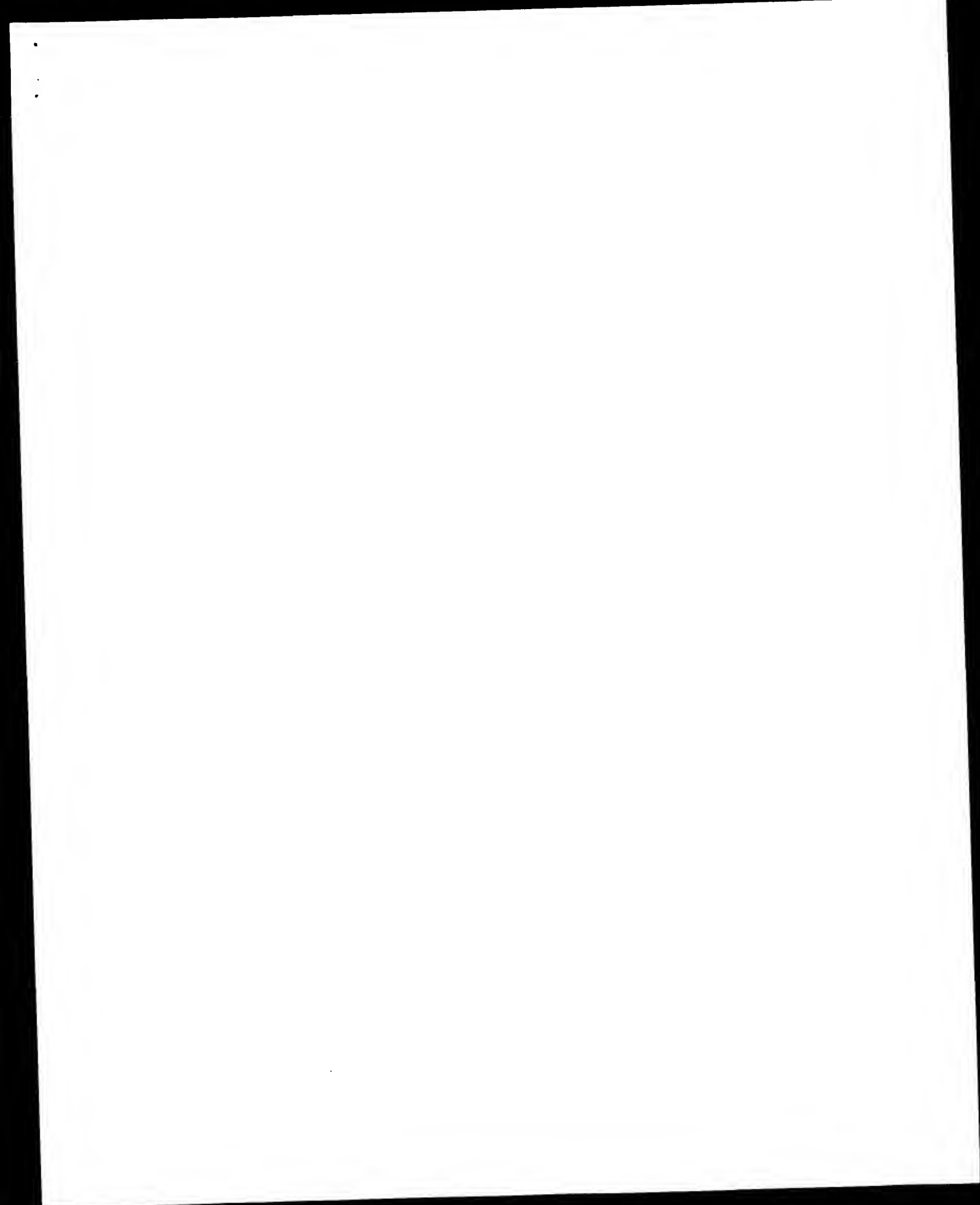
OY 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISLESQDASHDVEVLIILANN 120

DB 61 EDLQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISLESQDASHDVEVLIILANN 120

OY 121 SLSSNGVNTESGCKECEELEKNKEFLDSFVHIYDMFTNLS 162

DB 121 SLSSNGVNTESGCKECEELEKNKEFLDSFVHIYDMFTNLS 162

Search completed: February 20, 2003, 16:28:23
 Job time : 34 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 16:27:12 ; Search time 23.5 Seconds

(without alignments)
662,714 Million cell updates/sec

Title: US-09-855-313a-2

Perfect score: 835

Sequence: 1 MRISKPHLRISISICVCLL.....NIKEFLDSFVHIVDMFINTS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79.5	95.2	162	1	interleukin-15 pre
2	61.6	73.8	162	2	interleukin-15 - m
3	97.5	11.7	433	2	hypothetical prote
4	96	11.5	517	2	FUN26 protein - ye
5	86.5	10.4	500	2	hypothetical prote
6	85	10.2	510	2	NADH2 dehydrogenas
7	84	10.1	319	2	tryptophan-trna ii
8	84	10.1	928	2	hypothetical prote
9	82.5	9.9	477	2	N-ethylameline ch
10	82	9.8	1799	2	serine/threonine k
11	81.5	9.8	595	1	myb-related protei
12	81.5	9.8	642	2	hypothetical prote
13	80.5	9.6	922	2	hypothetical prote
14	80.5	9.6	1817	2	proliferase (proline
15	79.5	9.5	364	2	glutamine-fructose
16	79	9.5	456	2	glutamine-fructose
17	78.5	9.4	598	2	probable regulator
18	78.5	9.4	684	2	hypothetical prote
19	78	9.3	491	2	interleukin, probab
20	78	9.3	646	2	hypothetical prote
21	77.5	9.3	229	2	hypothetical prote
22	77.5	9.3	707	2	probable beta-adap
23	77.5	9.3	809	2	hypothetical prote
24	77.5	9.3	1113	2	hypothetical prote
25	77.5	9.3	3394	2	regulatory protein
26	77	9.2	520	2	regulatory protein
27	76.5	9.2	527	2	NADH2 dehydrogenas
28	76.5	9.2	810	2	protein PVI00 (imp
29	76	9.1	387	2	hypothetical prote

30	76	9.1	468	2	cytochrome P450 -
31	76	9.1	725	2	FUSION, Nucleoside
32	76	9.1	767	1	cdcl0 start contro
33	76	9.1	1070	2	exodeoxyribonuclea
34	76	9.1	1790	2	transport protein
35	75.5	9.0	521	2	DNA helicase Q1 in
36	75.5	9.0	729	2	JC3505
37	75.5	9.0	729	2	fibroblast growth
38	75.5	9.0	1353	2	hypothetical prote
39	75	9.0	307	2	hypothetical prote
40	75	9.0	820	2	acylttransferase (E
41	75	9.0	849	2	hypothetical prote
42	75	9.0	1021	2	hypothetical prote
43	74.5	8.9	365	2	connectin/citin -
44	74.5	8.9	447	2	probable MCP-type
45	74.5	8.9	572	2	Ca2+/calmodulin-de
					hypothetical prote

ALIGNMENTS

RESULT 1
A53484

interleukin-15 precursor - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A53484

R:Grubstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.;

Science 264, 965-968, 1994

A:Title: Cloning of a T cell growth factor that interacts with the beta chain of the

A:Reference number: A53484; MUID:94233380; PMID:8178155

A:Accession: A53484

A:Molecule type: mRNA

A:Status: nucleic acid sequence not shown

A:Residues: 1-162 <GRA>

A:Cross-references: GB:003099; NID:9493521; PIDN:AAAI8416.1; PID:9493522

A>Note: the complete translation is not shown

C:Keywords: growth factor

C:Keywords: interleukin-15

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

E:83-133,90-136/Disulfide bonds: #status predicted

11

Db 267 S-----DCKKLPVSLKNGCYCYIDEFKLEPIINLOKINISSN 306

RESULT 6

T11943

MADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - *Prototheca wickerhamii* mitochondrion
C:Species: *mitochondrion Prototheca wickerhamii*
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
R:Wolff, G.; Planke, I.; Lang, B.F.; Kueck, U.; Burger, G.
J. Mol. Biol. 237, 75-86, 1994

A:Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga *Prototheca*

A:Reference number: 217373; MUID:94180393; PMID:8133522
A:Accession: T11943

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-510 <MOL>

A:Cross-references: EMBL:U02970; NID:9467843; PID:9467875; PIDN:AA012662.1

A:Experimental source: strain 263-11

A:Genetics:

A:Note: nad2

A:Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C:Keywords: membrane associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match Best Local Similarity 10.2%; Score 85; DB 2; Length 510; Matches 18; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Db 157 LOSISFYVLAALKRSEFATAGKTFLLGAFSSCL 192

8 LRSTISQCYCLLNHFLFAGHVFILGCSAGL 43

RESULT 7

B81382

tryptophan-tRNA ligase (EC 6.1.1.2) Cj0388 (imported) - *Campylobacter jejuni* (strain NCCT)

C:Species: *Campylobacter jejuni*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
R:Parhill, J.; Wren, B.W.; Mungall, K.; Kelley, J.M.; Churcher, C.; Basham, D.; Chilling

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyf

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: B81382

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-319 <PAR>

A:Cross-references: GB:AL139075; GB:AL111168; NID:96967817; PIDN:CA874224.1; PID:9696786

A:Experimental source: serotype O2, strain NCCT 11168

C:Genetics:

A:Gene: trpS; Cj0388

C:Superfamily: tryptophan-tRNA ligase

C:Keywords: ligase

Query Match Best Local Similarity 10.1%; Score 84; DB 2; Length 319; Matches 39; Conservative 33; Mismatches 68; Indels 22; Gaps 7;

Db 142 VGKDOQWETARDAALAKVNMKEGFTLPPEARVNEAVAVGTDGAKMSKYONTIDIF 201

55 SDKKTIEDLQSMHIDATLTYSVDHPSCVTAM-KCFL-----LFLQVLSLSDGASIH 108

202 SSKRTLKQISSIVDSTALEDKDHENCNIFKIAKLFDESQOKLQIRIDKGBEGYGH 261

109 DTVENDILANSSLSNGNVTGSCGCELEEE-KNKKEFLD 149

262 -----FKYINLELV--NAYFKAREKYNLELKPSHUKETLD 296

RESULT 8

T04192

hypothetical protein T4P9.30 - *Arabidopsis thaliana*

N:Alternate names: protein T4P9.30

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

R:Bevan, M.; Medler, H.; Medler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K

submitted to the Protein Sequence Database, March 1999

A:Reference number: 215260

A:Accession: T04192

A:Molecule type: DNA

A:Residues: 1-928 <BPV>

A:Cross-references: EMBL:AL049523

A:Experimental source: cultivar Columbia; BAC clone T4P9

A:Genetics:

A:Map position: 4

A:Insertions: 51/2; 122/2; 161/3; 181/3; 214/3; 328/1; 401/3; 458/3; 544/3; 596/2; 774/2

A:Note: T4P9.30

Query Match Best Local Similarity 10.1%; Score 84; DB 2; Length 928; Matches 36; Conservative 25; Mismatches 54; Indels 24; Gaps 7;

Db 137 YTRSYSEVYPLCLMELTGRDSRTASIRELYEKVCMGTGVDERKHIDVDFDKRKGGL 196

56 D--LKKIEDLQSMHIDATLTYSVDHPSCVTAMKCFLEQVLSLSDGASIHDTVE 112

197 DPLYSKLEE--SSLHMDQDILVEYDGLSSSSQSSMSTGNEFLAVLEPS-----R 246

113 NLITLANSLSNGNVTES 131

247 SIYTAGCPTLNSGHSTPS 265

RESULT 9

T46666

N-ethylmaleine chlorohydrolase [validated] - *Rhodococcus corallinus*

N:Alternate names: s-triazine hydrolase

C:Species: *Rhodococcus corallinus*

C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000

R:Shao, Z.O.; Seftens, W.; Mulder, W.; Bekki, R.M.

J. Bacteriol. 177, 5748-5755, 1995

A:Title: Cloning and expression of the s-triazine hydrolase gene (trza) from *Rhodococ*

eridicde atrazine.

A:Reference number: 223125; MUID:96011356; PMID:7592318

A:Accession: T46666

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-477 <SHA>

A:Cross-references: EMBL:L16534; NID:9294669; PIDN:AAA90931.1; PID:9294671

A:Experimental source: tissue 11b NRRL 15444B

C:Genetics:

A:Gene: trza

C:Function:

A:Description: involved in atrazine degradation [validated, MUID:96011356]

C:Superfamily: Aquifex aeolicus N-ethylmaleine chlorohydrolase

Query Match Best Local Similarity 9.9%; Score 82.5; DB 2; Length 477; Matches 26; Conservative 22; Mismatches 41; Indels 21; Gaps 3;

Db 40 SAGLPRTKANM--VNVISDKKIEDLQSMHIDATLTYSVDHPSCVTAMKCFLEQ 96

321 TWGIGTDGANDSVNLISDMKVALIRAHARDASITPEKIIIMATIDGARCIDMADQ 380

97 VLSLESGDAS-----IHDTVENLIIILAN-----NSLSNGNV 128

381 IGSLEAGKRADIITLDIRHAGTTPRAHDLAATIVFOAYGNEVDVLYNGSV 430

RESULT 10

AD1895
serine/threonine kinase with two-component sensor domain alr0710 [imported] - Nostoc sp.
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AD1895
R:Kaneko, T.; Nakamura, Y.; Maki, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Itoh, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; M01D:21595285; PMID:11759840
A:Accession: AD1895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1799 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072667.1; PID:q17130055; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0710

Query Match 9.88; Score 82; DB 2; Length 1799;
Best Local Similarity 22.4%; Pred. No. 48; Indels 50; Gaps 7;
Matches 39; Conservative 27; Mismatches 58

36 LCGFSAGLPKTEANWVNSDLK-----KIEDLIOSMHIDATLYTESDVHSCCK 84
DB 1552 LGFTSATLQGTAKNADITELKLYENLENNREIOPHAKEMDPLF---EDLPKID 1608
QY 85 VTAKCFLE-----IQVLSGSD-----ASIDHYENILILANSSLSN----- 125
DB 1609 AMIACNRLNISTSLRFSRADNDYKKNALGEGDSTILILKRLKMOOHPALEVIT 1668
QY 126 -GNVTEGSC-----KECELEEKNT-KEFLDSFHYIDMFINTS 162
DB 1669 NYGDLPLVNCFCPOLNQVEMILANALALEANIGKSAETIHPRIITTS 1722

RESULT 11

AA8077
myb-related protein REB1 - yeast (Kluyveromyces marxianus var. lactis)
C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: AA8077
R:Morrow, B.E.; Ju, O.; Warner, J.R.
Mol. Cell. Biol. 13, 1173-1182, 1993
A:Title: A bipartite DNA-binding domain in yeast Reb1p.
A:Reference number: AA8077; M01D:93140755; PMID:8423784
A:Accession: AA8077
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-599 <MOR>
A:Cross-references: GB:U03789; NID:q173313; PIDN:AA61343.1; PID:q173314
A:Note: sequence extracted from NCBI database (NCBI:123574, NCBI:123576)
C:Superfamily: myb-related protein REB1; myb DNA-binding repeat homology
C:Keywords: DNA binding; nucleus; transcription regulation
F:333-382/Domain: myb DNA-binding repeat homology <MOR>

Query Match 9.88; Score 81.5; DB 1; Length 595;
Best Local Similarity 25.0%; Pred. No. 14;
Matches 28; Conservative 23; Mismatches 52; Indels 9; Gaps 2;

QY 44 PTEANWVNSDLKIEDLIOSMHIDATLYTESDVHSCVTKMKCFLELVISLSSG 103
DB 183 PKKESERSYGLSDIHDVDSVSGSIPSOYRLKTAELP-----KVLSSSEH 234
QY 104 DASIDHYENILILANSSLSNGN-VTESGCKECELLEKNIKELFSDPVHI 154
DB 235 NDDQDDVSNLIGFAAKASHIINPATOSNGKSFDESEEALEDFIREYOKI 286

RESULT 12

T28866
hypothetical protein R03H4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Nov-2000
C:Accession: T28866
R:Brashaw, H.
Submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid R03H4.
A:Reference number: Z20534
A:Accession: T28866
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-642 <BRA>
A:Cross-references: EMBL:U50300; PIDN:AC48109.1; GSPDB:GN00023; CESP:R03H4.1
A:Experimental source: strain Bristol N2; clone R03H4
C:Genetics:
A:Gene: CESP:R03H4.1
A:Map position: 5
A:Insertions: 35/2; 66/2; 123/3; 166/3; 280/3; 321/1; 419/3; 460/1; 495/2; 586/3
C:Superfamily: Caenorhabditis elegans hypothetical protein T26H2.7

Query Match 9.88; Score 81.5; DB 2; Length 642;
Best Local Similarity 24.3%; Pred. No. 16;
Matches 33; Conservative 28; Mismatches 56; Indels 19; Gaps 6;

QY 22 NSHFLTEAGIHVFLIGCFSGALPKTEANWVNSDLKIEDLIOSMHIDATLYTESDVH 80
DB 517 NIQFYISAKKIYILGSH---PLVNIHNLNLFILYLIQNSDELISLHNR---FKRDD 569
QY 81 PSC-----KYAMKCFLELVISLSSGDSIHDTVENILILANSSLSNGVTEGCK 134
DB 570 MRCVKRRKFKYKCKCKQFFLSHYFV-CDKYLFPDRSLISYVDWI---HILTSAGK 624
QY 135 ECELEEKNIKEFLDS 150
DB 625 ICGPVFENLAKELMNN 640

RESULT 13

T03854
hypothetical protein CO2A12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T03854
R:Geisler, C.; Kramer, J.; Smith, A.; Elliott, G.; O'Brien, D.
Submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid CO2A12.
A:Reference number: Z16067
A:Accession: T03854
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-922 <WIL>
A:Cross-references: EMBL:AF016415; NID:q2291123; PIDN:AA65265.1; PID:q2291126
A:Map position: V
A:Insertions: 35/2; 66/2; 123/3; 179/3; 290/3; 331/1; 434/3; 475/1; 510/2; 603/3; 658/2;
A:Note: CO2A12.2

Query Match 9.66; Score 80.5; DB 2; Length 922;
Best Local Similarity 25.2%; Pred. No. 30;
Matches 31; Conservative 24; Mismatches 43; Indels 25; Gaps 7;

QY 33 VFILIGFSAGLPKTEANWVNSDLKIEDLIOSMHIDATLYTESDV-----HP 81
DB 543 VFILIG-----ALPYFVNLNLFILYLIQNSDELISLHNR---ADDVYNEKRELAER 597
QY 82 SCXYTAKKCFLELVISLSSGDSIHDTVENILILANSSLSNGVTEGCKECELLE 141
DB 598 RCK-----KQFIDNLFLELKGKVLTFD--RNSLL---SYLDNGHLMPPAVKLEPILF 648
QY 142 KNI 144

Db 649 KTI 651

RESULT 14

T10689

hypothetical protein T16118.30 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999

R:Bevan, M.; Leonard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16533

A:Accession: T10689

A:Molecule type: DNA

A:Residues: 1-1817 <BEV>

A:Cross-references: EMBL:AL049915; GSPDB:GN00062; ATSP:T16118.30

A:Experimental source: cultivar Columbia; BAC clone T16118

C:Genetics:

A:Gene: ATSP:T16118.30

A:Map position: 4

A:Introns: 1/3; 26/3; 66/3; 80/2; 151/1; 745/3; 786/3; 976/3; 1045/1; 1120/1; 1155/3; 12

Query Match

Best Local Similarity 9.6%; Score 80.5; DB 2; Length 1817;

Matches 47; Conservative 25; Mismatches 63; Indels 65; Gaps 8;

QY 3 ISKPHLR-----SISIOCYCLILNSHFLTEAGT-----HYFLGCFSGALP-----44

Db 585 IORPHCRVRELTINRIHEINILKIDFLENNIPEMKEKEFYSECVNLAPLFPDKD1 644

QY 45 -----KTFANWVVISDLKIFDL---OSMHIDATLYTESDVHPSCVTAMKCFLE 94

Db 645 LPAYAVKTBEGISSV--EISALEVLKACOKRKPIDVEY-----MNCRRK 689

QY 95 LOVT-----SLESGDASIHDTVENLIL---ANNSLSNNGWTEG 132

Db 690 LQYLDSTGTGESVYTPKTSKNSSEMDHLVAEYKAILLCISOVKNLSDSGNSRYS 749

QY 133 CKECELEEKIKKEPLDSFV 152

Db 750 SONADGIEEKKSCFIDAKI 769

QY 750 SONADGIEEKKSCFIDAKI 769

Db 750 SONADGIEEKKSCFIDAKI 769

QY 750 SONADGIEEKKSCFIDAKI 769

Db 750 SONADGIEEKKSCFIDAKI 769

QY 750 SONADGIEEKKSCFIDAKI 769

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Db 750 SONADGIEEKKSCFIDAKI 769

QY 750 SONADGIEEKKSCFIDAKI 769

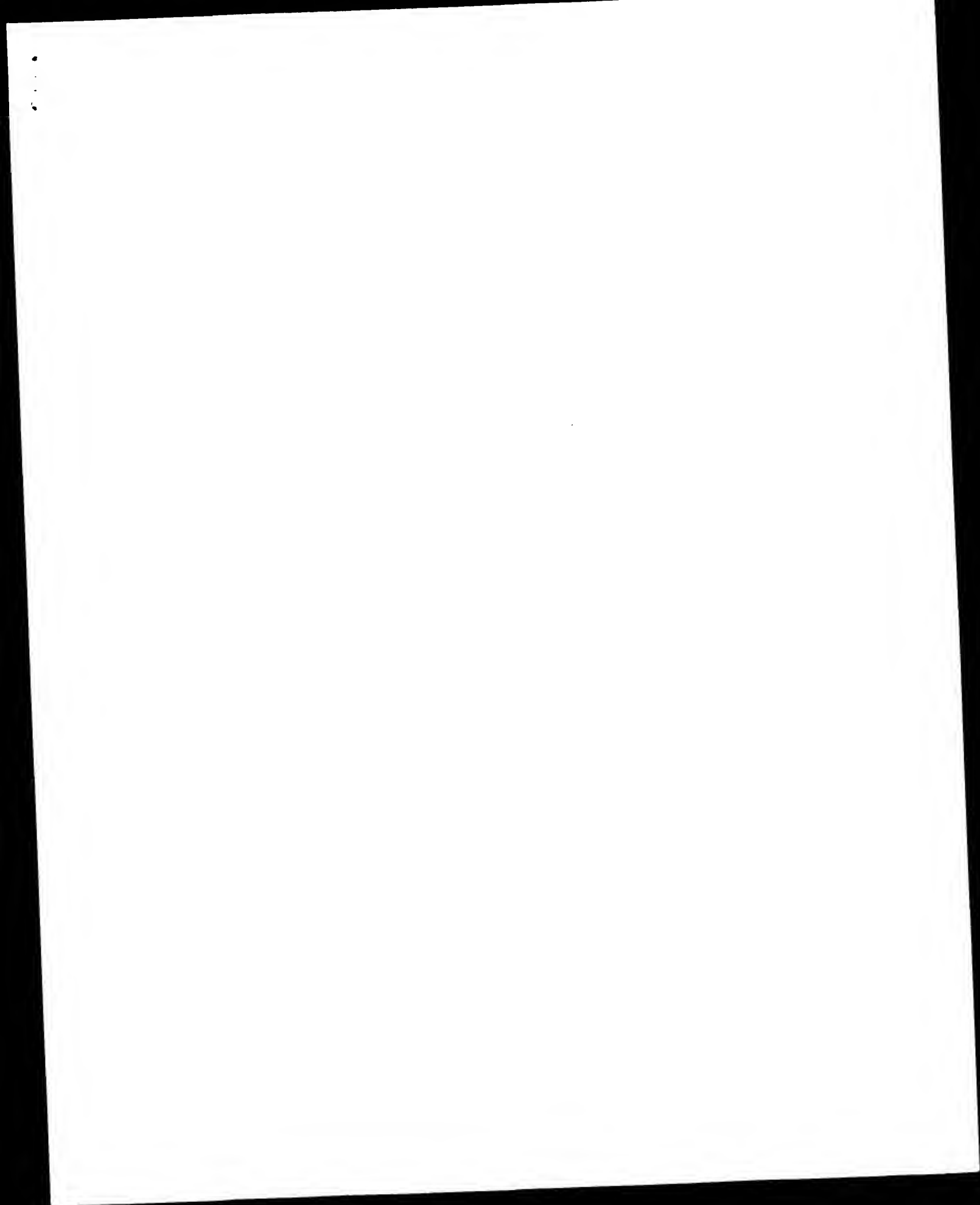
Db 750 SONADGIEEKKSCFIDAKI 769

Db 92 KNAVALTSCIVEAPRLTYARQVALDAPFAIKLIDGPEFLMELR-----KOKSAKELMTLK 147

QY 113 NLILANNSLSNNGWTEGCKE-----ELEKRNKE 146

Db 148 EAAALADYGVGVQVATQEGREFFILALIEYELKRGVARD 188

Search completed: February 20, 2003, 16:32:08
 Job time: 26.5 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 20, 2003, 16:27:07; Search time 16.5 Seconds
(without alignments)
407.222 Million cell updates/sec

Title: US-09-855-313a-2

Perfect score: 835

Sequence: 1 MRSLKPHLSISIOCYICLL.....NIKEFLDSFVHIYDNFINIS 162

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	823	98.6	162	1 IL15_HUMAN	P40933 homo sapien
2	800	95.8	162	1 IL15_HUMAN	P48092 macaca mla
3	795	95.2	162	1 IL15_CERAE	P40221 cercopithec
4	680	81.4	162	1 IL15_FELCA	097687 felis silve
5	655	78.4	162	1 IL15_PIG	095253 sus scrota
6	645	77.2	162	1 IL15_BOVIN	028028 bos taurus
7	634	77.0	162	1 IL15_SHEEP	09x516 ovis aries
8	616	73.8	162	1 IL15_MOUSE	P48346 mus musculu
9	607	72.7	162	1 IL15_RAT	P97604 rattus norv
10	96	11.5	517	1 F026_YEAST	P31811 saccharomyc
11	82.5	9.9	517	1 TRZA_RHOCO	052725 rhodococcus
12	81.5	9.8	595	1 REBL_KIULA	005950 kluyveromyc
13	81	9.7	269	1 TRPA_BUCSC	046004 buchnera ap
14	79	9.5	456	1 R1N1_RAT	P29315 rattus norv
15	78.5	9.4	340	1 HEM3_CANAL	P56826 sepi offic
16	78.5	9.4	340	1 HEM3_CANAL	094048 candida alb
17	78.5	9.4	340	1 HEM3_CANAL	094048 candida alb
18	78.5	9.4	340	1 HEM3_CANAL	094048 candida alb
19	78.5	9.4	340	1 HEM3_CANAL	094048 candida alb
20	77.5	9.3	707	1 USOL_YEAST	P25386 saccharomyc
21	77.5	9.3	707	1 USOL_YEAST	P25386 saccharomyc
22	77.5	9.3	707	1 USOL_YEAST	P25386 saccharomyc
23	76	9.2	527	1 ADDB_YEAST	P47166 saccharomyc
24	76	9.1	490	1 NU2M_ACACA	P46682 saccharomyc
25	76	9.1	491	1 HSP1_CHICK	P33526 gallus galli
26	76	9.1	491	1 HSP1_CHICK	P33526 gallus galli
27	75.5	9.0	1070	1 IM44_HUMAN	P01129 schizosacch
28	75.5	9.0	1070	1 IM44_HUMAN	P01129 schizosacch
29	75.5	9.0	1070	1 IM44_HUMAN	P01129 schizosacch
30	75.5	9.0	1070	1 IM44_HUMAN	P01129 schizosacch
31	74.5	8.9	447	1 KCC2_YEAST	P22317 saccharomyc
32	74.5	8.9	447	1 KCC2_YEAST	P22317 saccharomyc
33	74.5	8.9	447	1 KCC2_YEAST	P22317 saccharomyc
34	74.5	8.9	447	1 KCC2_YEAST	P22317 saccharomyc

ALIGNMENTS

34	74	8.9	668	1	V244_F0MPV	O91426 fowlpox vir
35	74	8.9	938	1	V120_HSV1J	P52438 human herpe
36	73.5	8.8	521	1	IMA3_HUMAN	000505 homo sapien
37	73.5	8.8	521	1	IMA3_MOUSE	035344 mus musculu
38	73	8.7	497	1	NU2M_CHOIR	P48903 chondrus cr
39	73	8.7	497	1	PGHM_HUMAN	P28160 homo sapien
40	72.5	8.7	791	1	ION_CAMJE	069300 campylobact
41	72.5	8.7	807	1	PTNM_HUMAN	Q9Y212 homo sapien
42	72	8.6	364	1	PYRC_YEAST	P20051 saccharomyc
43	71.5	8.6	355	1	HIS7_BUCAP	Q92he4 buchnera ap
44	71.5	8.6	384	1	GRR_HUMAN	P30550 homo sapien
45	71.5	8.6	456	1	RINI_PIG	P10775 sus scrota

RESULT 1

IL15_HUMAN STANDARD: PRT: 162 AA.

AC P40933; Q93058; 043512; 000440; Q90BA3;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DE Interleukin-15 precursor (IL-15).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

SEQUENCE FROM N.A. (IL15-S48A ISOFORM).

RA Grabstein K.K., Eisenman J., Sheenebeck K., Rauch C.,

RA Srinivasan S., Fung V., Beers C., Richardson J., Schenborn M.A.,

RA Andiegh M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,

RA Giti U.G.;

RA "Cloning of a T cell growth factor that interacts with the beta chain

of the interleukin-2 receptor.";

Science 264:965-968(1994).

SEQUENCE FROM N.A. (IL15-S21AA ISOFORM).

RA Krause H., Jandrig B., Wernicke C., Bullone-Paus S., Pohl T.,

RA Diamantstein T.;

RA Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A. (IL15-S21AA ISOFORM).

RA TISSUE=Lung cancer;

RA MEDLINE=96218668; PubMed=6668345;

RA Meazza R., Verdiani S., Blassoni R., Coppolecchia M., Gaggero A.,

RA Orongo A.M., Colombo M.P., Azzone B., Ferrini S.;

RA "Identification of a novel interleukin-15 (IL-15) transcript isoform

generated by alternative splicing in human small cell lung cancer

cell lines.";

Oncogene 12:2187-2192(1996).

34	74	8.9	668	1	V244_F0MPV	O91426 fowlpox vir
35	74	8.9	938	1	V120_HSV1J	P52438 human herpe
36	73.5	8.8	521	1	IMA3_HUMAN	000505 homo sapien
37	73.5	8.8	521	1	IMA3_MOUSE	035344 mus musculu
38	73	8.7	497	1	NU2M_CHOIR	P48903 chondrus cr
39	73	8.7	497	1	PGHM_HUMAN	P28160 homo sapien
40	72.5	8.7	791	1	ION_CAMJE	069300 campylobact
41	72.5	8.7	807	1	PTNM_HUMAN	Q9Y212 homo sapien
42	72	8.6	364	1	PYRC_YEAST	P20051 saccharomyc
43	71.5	8.6	355	1	HIS7_BUCAP	Q92he4 buchnera ap
44	71.5	8.6	384	1	GRR_HUMAN	P30550 homo sapien
45	71.5	8.6	456	1	RINI_PIG	P10775 sus scrota

SEQUENCE OF 49-162 FROM N.A.

"Expression of two IL-15 mRNA isoforms in human tumors does not

correlate with secretion: role of different signal peptides.";

Proc. Natl. Acad. Sci. U.S.A. 94:1444-1449(1997).

[5]

SEQUENCE FROM N.A. (ISOFORM 3).

RA Meazza R., Ferrini S.;

RA "Expression of two IL-15 mRNA isoforms in human tumors does not

correlate with secretion: role of different signal peptides.";

Proc. Natl. Acad. Sci. U.S.A. 94:1444-1449(1997).

[6]

SEQUENCE OF 49-162 FROM N.A.

IL15_CERAE
ID IL15_CERAE STANDARD: PRT: 162 AA.
AC P40221;
DT 01-FEB-1995 (Rel. 31, Created)
DE Interleukin-15 precursor (IL-15).
GN IL15.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 49-81.
RC TISSUE=Kidney;
RX MEDLINE=9423380; PubMed=8178155;
RA Grabstein K.H., Eisenman J., Shanebeck K., Rauch C.,
RA Srinivasan S., Fung V., Beers C., Richardson J., Schoenborn M.A.,
RA Adhieh M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,
RA Gird J.G.;
RT *Cloning of a T cell growth factor that interacts with the beta chain
RT of the interleukin-2 receptor.*;
RL Science 264:965-968(1994).
CC -! FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC GAMMA BUT NOT IL-2R ALPHA.
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! SIMILARITY: BELONGS TO THE IL-15 FAMILY.
CC
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CC
CC EMBL: U03099; AAI8416.1;
CC InterPro: IPR003443; Interleukin_15.
CC Pfam: PF02372; IL15; I.
CC KW Cytokine; Glycoprotein; Signal.
CC FT SIGNAL 1 29 POTENTIAL.
CC FT PROPEP 30 48
CC FT CHAIN 49 162 INTERLEUKIN-15.
CC FT DISULFID 83 133 POTENTIAL.
CC FT DISULFID 90 136 POTENTIAL.
CC FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).
CC SO SEQUENCE 162 AA; 18222 MW; 1BF9A82644E1C9B7 CMC64;
Query Match 95.2%; Score 795; DB 1; Length 162;
Best Local Similarity 95.1%; Pred. No. 6, 9e-65;
Matches 154; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 MRISPRHSISIOCTYCLLSHFLTEAGIHVILGCFSAGLPTEANNVWVISDLKTI 60
DB 1 MRISPRHSISIOCTYCLLSHFLTEAGIHVILGCFSAGLPTEANNVWVISDLKTI 60
QY 61 EDLIOSMHIDATLTYESDVHPSCKVTAMKCFLELOVISLSSGASIHDTVENLIITANN 120
DB 61 EDLIOSMHIDATLTYESDVHPSCKVTAMKCFLELOVISLSSGASIHDTVENLIITANN 120
QY 121 SLSSNCWNTESGCKECELLEKNIKEFLDSFVHIYDMFINTS 162
DB 121 SLSSNCWNTESGCKECELLEKNIKEFLDSFVHIYDMFINTS 162
QY 121 ILSSNNTITESGCKECELLEKNIKEFLDSFVHIYDMFINTS 162
DB 121 ILSSNNTITESGCKECELLEKNIKEFLDSFVHIYDMFINTS 162
RESULT 4
IL15_FELCA
ID IL15_FELCA STANDARD: PRT: 162 AA.
AC 097687;
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-15 precursor (IL-15).
GN IL15.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Barger A.B., Dean G.A., Lavoy A.S.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! SIMILARITY: BELONGS TO THE IL-15 FAMILY.
CC
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CC
CC EMBL: AF108148; AAD05268.1;
CC InterPro: IPR003443; Interleukin_15.
CC Pfam: PF02372; IL15; I.
CC KW Cytokine; Glycoprotein; Signal.
CC FT SIGNAL 1 29 POTENTIAL.
CC FT PROPEP 30 48
CC FT CHAIN 49 162 INTERLEUKIN-15.
CC FT DISULFID 83 133 POTENTIAL.
CC FT DISULFID 90 136 POTENTIAL.
CC FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).
CC SO SEQUENCE 162 AA; 18412 MW; D8C7CEFFFA0110DD CMC64;
Query Match 81.4%; Score 680; DB 1; Length 162;
Best Local Similarity 81.5%; Pred. No. 1, 6e-54;
Matches 132; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
QY 1 MRISPRHSISIOCTYCLLSHFLTEAGIHVILGCFSAGLPTEANNVWVISDLKTI 60
DB 1 MRISPRHSISIOCTYCLLSHFLTEAGIHVILGCFSAGLPTEANNVWVISDLKTI 60
QY 61 EDLIOSMHIDATLTYESDVHPSCKVTAMKCFLELOVISLSSGASIHDTVENLIITANN 120
DB 61 EDLIOSMHIDATLTYESDVHPSCKVTAMKCFLELOVISLSSGASIHDTVENLIITANN 120
QY 121 SLSSNCWNTESGCKECELLEKNIKEFLDSFVHIYDMFINTS 162
DB 121 SLSSNCWNTESGCKECELLEKNIKEFLDSFVHIYDMFINTS 162
QY 121 ILSSNNTITESGCKECELLEKNIKEFLDSFVHIYDMFINTS 162
DB 121 ILSSNNTITESGCKECELLEKNIKEFLDSFVHIYDMFINTS 162
RESULT 5
IL15_PIG
ID IL15_PIG STANDARD: PRT: 162 AA.
AC 095253;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Interleukin-15 precursor (IL-15).
GN IL15.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.

CC TISSUE-Blood;
 CC MEDLINE=9749311; PubMed=9305780;
 CC RA Canals A., Grimm D.R., Gasbarre L.C., Lunney J.K., Zarlega D.S.;
 CC RT "Molecular cloning of cDNA encoding porcine interleukin-15."
 CC RL Gene 195:337-339(1997).
 CC CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 CC GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
 CC CC CELLULAR LOCATION: Secreted.
 CC CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
 CC CC -----
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 CC -----
 CC DR EMBL: U58142; AAB72031.1; -
 CC DR InterPro: IPR003443; Interleukin_15.
 CC DR Pfam: PF02372; IL15; 1.
 CC CC Cytokine; Glycoprotein; Signal.
 CC FT SIGNAL 1 29 POTENTIAL.
 CC FT PROPEP 30 48 INTERLEUKIN-15.
 CC FT CHAIN 49 162 POTENTIAL.
 CC FT DISULFID 83 133 POTENTIAL.
 CC FT CARBOHYD 90 136 POTENTIAL.
 CC FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 162 AA; 18437 MW; 7EF7992391883446 CRC64;
 CC SQ SEQUENCE
 CC
 CC Query Match 78.4%; Score 655; DB 1; Length 162;
 CC Best Local Similarity 80.2%; Pred. No. 2.8e-52;
 CC Matches 130; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
 CC
 CC QY 1 MRISPHLRISIQCYICLLNSHPTLEAGIHVFLIGCFSGAGLPKTEAMWVNSDLKTI 60
 CC DB 1 MRLKPLRLSTQCYICLLNSHPTLEAGIHVFLIGCFSGAGLPKTEAMWVNSDLKTI 60
 CC QY 61 EDLIQSHMDATLTYESDVHPSCVTKAMKCFLELOVLSLESGASIHDTVENLIILANN 120
 CC DB 61 EDLIQSHMDATLTYESDVHPSCVTKAMKCFLELOVLSLESGASIHDTVENLIILANN 120
 CC QY 121 SLSNGVNTESGKECELEEKNIKEFLDSFVHYDMFINTS 162
 CC DB 121 SLSNGVNTESGKECELEEKNIKEFLDSFVHYDMFINTS 162
 CC
 CC RESULT 6
 CC ID IL15_BOVIN STANDARD: PRT: 162 AA.
 CC AC Q28028;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
 CC DE Interleukin-15 precursor (IL-15).
 CC CN IL15.
 CC OS Bos taurus (Bovine).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Bovinae; Bos.
 CC OX NCBI_TaxID=9913;
 CC RN (1)
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Holstein;
 CC RA MEDLINE=97426124; PubMed=9282828;
 CC RA Canals A., Gasbarre L.C., Boyd P.C., Almeria S., Zarlega D.S.;
 CC RT "Cloning and expression of bovine interleukin-15: analysis and
 CC modulation of transcription by exogenous stimulation."
 CC RL J. Interferon Cytokine Res. 17:473-480(1997).
 CC CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15

CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 CC GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
 CC CC -1- SUBCELLULAR LOCATION: Secreted.
 CC CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
 CC CC -----
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 CC -----
 CC DR EMBL: U42433; AAB5130.1; -
 CC DR InterPro: IPR003443; Interleukin_15.
 CC DR Pfam: PF02372; IL15; 1.
 CC CC Cytokine; Glycoprotein; Signal.
 CC FT SIGNAL 1 29 POTENTIAL.
 CC FT PROPEP 30 48 INTERLEUKIN-15.
 CC FT CHAIN 49 162 POTENTIAL.
 CC FT DISULFID 83 133 POTENTIAL.
 CC FT CARBOHYD 90 136 POTENTIAL.
 CC FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 113 113 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 121 121 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 162 AA; 18554 MW; 6A63CA329EB8302 CRC64;
 CC SQ SEQUENCE
 CC
 CC Query Match 77.2%; Score 645; DB 1; Length 162;
 CC Best Local Similarity 77.8%; Pred. No. 2.2e-51;
 CC Matches 126; Conservative 16; Mismatches 20; Indels 0; Gaps 0;
 CC
 CC QY 1 MRISPHLRISIQCYICLLNSHPTLEAGIHVFLIGCFSGAGLPKTEAMWVNSDLKTI 60
 CC DB 1 MRLKPLRLSTQCYICLLNSHPTLEAGIHVFLIGCFSGAGLPKTEAMWVNSDLKTI 60
 CC QY 61 EDLIQSHMDATLTYESDVHPSCVTKAMKCFLELOVLSLESGASIHDTVENLIILANN 120
 CC DB 61 EDLIQSHMDATLTYESDVHPSCVTKAMKCFLELOVLSLESGASIHDTVENLIILANN 120
 CC QY 121 SLSNGVNTESGKECELEEKNIKEFLDSFVHYDMFINTS 162
 CC DB 121 SLSNGVNTESGKECELEEKNIKEFLDSFVHYDMFINTS 162
 CC
 CC RESULT 7
 CC ID IL15_SHEEP STANDARD: PRT: 162 AA.
 CC AC Q9XST6;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Interleukin-15 precursor (IL-15).
 CC CN IL15.
 CC OS Ovis aries (Sheep).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Caprinae; Ovis.
 CC OX NCBI_TaxID=9940;
 CC RN (1)
 CC RP SEQUENCE FROM N.A.
 CC RC CASEY G.J., CHAPLIN P.J.;
 CC RA "Isolation of interleukin-15 mRNA transcripts from T and B cells
 CC circulating in effluent lymph."
 CC RT J. Interferon Cytokine Res. 0:0-0(1999).
 CC RL -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 CC GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
 CC CC -1- SUBCELLULAR LOCATION: Secreted.
 CC CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
 CC CC -----
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DR EMBL: A149700; AAD37425.1;
 DR InterPro: IPR003443; Interleukin_15.
 DR Pfam: PF02372; IL15: 1.
 KW Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 48 POTENTIAL.
 FT CHAIN 49 162 INTERLEUKIN-15.
 FT DISULFID 83 133 POTENTIAL.
 FT DISULFID 90 136 POTENTIAL.
 FT CARBOHYD 113 113 N-LINKED (GLCNAC: . . .) (POTENTIAL).
 FT CARBOHYD 121 121 N-LINKED (GLCNAC: . . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC: . . .) (POTENTIAL).
 SQ SEQUENCE 162 AA; 18510 MW; 87195650E45F1E5D CRC64;

Query Match
 Best Local Similarity 77.0%; Score 643; DB 1; Length 162;
 Matches 123; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 MRISPHLRSTISQCYCLINSHFLTEAGIHVFLIGCFSGALPKRTANWVYISDLKRI 60
 DB 1 MKILKPYLRSTISQCYCLINSHFLTEAGIHVFLIGCFSGALPKRTANWVYISDLKRI 60
 QY 61 EDLIQSHMDATLYTESDVHPSCKVTAAMKCFLELOVTSLESGDASIHDTVENLITLANN 120
 DB 61 EDLIQSHMDATLYTESDVHPSCKVTAAMKCFLELOVTSLESGDASIHDTVENLITLANN 120
 QY 121 SLSSNGVTVESGCKCEELFEKNIKEFLDSFVHIYDMFINTS 162
 DB 121 SLSSNGVTVESGCKCEELFEKNIKEFLDSFVHIYDMFINTS 162
 QY 121 TSSSNKVAESGCKCEELFEKNIKEFLDSFVHIYDMFINTS 162
 DB 121 TSSSNKVAESGCKCEELFEKNIKEFLDSFVHIYDMFINTS 162

RESULT 8
 IL15_MOUSE

ID IL15_MOUSE STANDARD: PRT; 162 AA.
 AC P48346;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-15 precursor (IL-15).
 GN IL15.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=WC/REJ X C57BL/6J; TISSUE=Bone marrow;
 RA MEDLINE=95278940; PubMed=7759105;
 RA Anderson D.M., Johnson L., Glaccum M.B., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Valentine V., Kirstein M.N., Shapiro D.N., Morris S.W.,
 RA Grabstein K., Cosman D.;
 Chromosomal assignment and genomic structure of IL15.
 RT Genomics 25:701-706(1995).

CC -I- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 CC GAMMA BUT NOT IL-2R ALPHA.
 CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- SIMILARITY: BELONGS TO THE IL-15 FAMILY.

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DR EMBL: U14332; AAA75377.1;
 DR MGI: 103014; 1115.
 DR InterPro: IPR003443; Interleukin_15.
 DR Pfam: PF02372; IL15: 1.
 KW Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 48 POTENTIAL.
 FT CHAIN 49 162 INTERLEUKIN-15.
 FT DISULFID 83 133 POTENTIAL.
 FT DISULFID 90 136 POTENTIAL.
 FT CARBOHYD 104 104 N-LINKED (GLCNAC: . . .) (POTENTIAL).
 FT CARBOHYD 108 108 N-LINKED (GLCNAC: . . .) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC: . . .) (POTENTIAL).
 SQ SEQUENCE 162 AA; 18593 MW; 68C971498CEBP296 CRC64;

Query Match
 Best Local Similarity 73.8%; Score 616; DB 1; Length 162;
 Matches 116; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 1 MRISPHLRSTISQCYCLINSHFLTEAGIHVFLIGCFSGALPKRTANWVYISDLKRI 60
 DB 1 MKILKPYLRSTISQCYCLINSHFLTEAGIHVFLIGCFSGALPKRTANWVYISDLKRI 60
 QY 61 EDLIQSHMDATLYTESDVHPSCKVTAAMKCFLELOVTSLESGDASIHDTVENLITLANN 120
 DB 61 EDLIQSHMDATLYTESDVHPSCKVTAAMKCFLELOVTSLESGDASIHDTVENLITLANN 120
 QY 121 SLSSNGVTVESGCKCEELFEKNIKEFLDSFVHIYDMFINTS 162
 DB 121 SLSSNGVTVESGCKCEELFEKNIKEFLDSFVHIYDMFINTS 162
 QY 121 TSSSNKVAESGCKCEELFEKNIKEFLDSFVHIYDMFINTS 162
 DB 121 TSSSNKVAESGCKCEELFEKNIKEFLDSFVHIYDMFINTS 162

RESULT 9
 IL15_RAT

ID IL15_RAT STANDARD: PRT; 162 AA.
 AC P97604; O54847;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Interleukin-15 precursor (IL-15).
 GN IL15.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]

RP SEQUENCE FROM N.A. (LONG FORM).
 RC STRAIN=Sprague-Dawley; TISSUE=Jejunum;
 RA MEDLINE=97098212; PubMed=8942753;
 RA Reinecker H.C., Macdermott R.P., Miran S., Dignass A., Podolsky D.K.;
 RA "Intestinal epithelial cells both express and respond to interleukin
 RA 15.*"
 RT Gastroenterology 111:1706-1713(1996).

CC -I- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 CC GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- SIMILARITY: BELONGS TO THE IL-15 FAMILY.

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 CC -----
 CC EMBL: U69272: AAB41697.1: -
 CC EMBL: AF015719: AAB94536.1: -
 CC EMBL: AF015718: AAB94535.1: -
 CC DR InterPro: IPR003443: Interleukin_15.
 CC DR Pfam: PF02372: IL15: 1.
 CC DR Cytokine: Glycoprotein; Signal: Alternative splicing.
 CC KW SIGNAL: 1
 CC FT PROPEP 30 48 POTENTIAL.
 CC FT CHAIN 49 162 INTERLEUKIN-15.
 CC FT DISULFID 83 133 POTENTIAL.
 CC FT DISULFID 90 136 POTENTIAL.
 CC FT CARBOHYD 10 10 N-LINKED (GLCNAC: .) (POTENTIAL).
 CC FT CARBOHYD 104 104 N-LINKED (GLCNAC: .) (POTENTIAL).
 CC FT CARBOHYD 108 108 N-LINKED (GLCNAC: .) (POTENTIAL).
 CC FT CARBOHYD 119 113 N-LINKED (GLCNAC: .) (POTENTIAL).
 CC FT CARBOHYD 143 143 N-LINKED (GLCNAC: .) (POTENTIAL).
 CC FT VARSPLIC 81 96 MISSING (IN SHORT ISOFORM).
 CC SQ SEQUENCE 162 AA: 18804 MW: DAB6097A0305AFA CRC64;
 CC
 CC Query Match 72.7%: Score 607; DB 1; Length 162;
 CC Best Local Similarity 71.0%: Pred. No. 5.9e-48;
 CC Matches 115; Conservative 20; Mismatches 27; Indels 0; Gaps 0;
 CC
 CC QY 1 MRISKPHLRISITQICLLINSHFLTEAGIHVFLIGCFSGAGLPKTEANVNVISDLKRI 60
 CC 1 MKRLKPYMRNTSLIYLICPLNSHFLTEAGIHVFLIGCFSGAGLPKTEANVNVISDLKRI 60
 CC 1 KRLKPYMRNTSLIYLICPLNSHFLTEAGIHVFLIGCFSGAGLPKTEANVNVISDLKRI 60
 CC DB 61 EDLIQSMHIDATYTESDVNPSCKVTAMKCFLELOVLSLGGASIHDPVENLLIANN 120
 CC 61 EDLIQSMHIDATYTESDVNPSCKVTAMKCFLELOVLSLGGASIHDPVENLLIANN 120
 CC 61 EDLIQSMHIDATYTESDVNPSCKVTAMKCFLELOVLSLGGASIHDPVENLLIANN 120
 CC DB 61 EDLIQSMHIDATYTESDVNPSCKVTAMKCFLELOVLSLGGASIHDPVENLLIANN 120
 CC QY 121 SISSNGNNTSESGKCECELEEKKEFLDSEFVHI VDMFTINS 162
 CC 121 SISSNGNNTSESGKCECELEEKKEFLDSEFVHI VDMFTINS 162
 CC 121 SISSNGNNTSESGKCECELEEKKEFLDSEFVHI VDMFTINS 162
 CC DB 121 SISSNGNNTSESGKCECELEEKKEFLDSEFVHI VDMFTINS 162
 CC QY 121 SISSNGNNTSESGKCECELEEKKEFLDSEFVHI VDMFTINS 162
 CC 121 SISSNGNNTSESGKCECELEEKKEFLDSEFVHI VDMFTINS 162
 CC 121 SISSNGNNTSESGKCECELEEKKEFLDSEFVHI VDMFTINS 162
 CC DB 121 SISSNGNNTSESGKCECELEEKKEFLDSEFVHI VDMFTINS 162
 CC RESULT 10
 CC FU26_YEAST STANDARD; PRT: 517 AA.
 CC ID FU26_YEAST
 CC AC P31381:
 CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
 CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Nucleoside transporter FUN26.
 CC GN FUN26 OR YAL022C.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CC OK NCBI_TaxID=4932;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=SB288C / AB972;
 CC RA MEDLINE=93209532; PubMed=8458570;
 CC RA Ouellette B.F., Clark M.W., Keng T., Storms R.K., Zhong W.W.,
 CC Zeng B., Fortin N., Delaney S., Barton A.B., Kaback D.B., Bussey H.;
 CC "Sequencing of chromosome I from Saccharomyces cerevisiae: analysis
 CC of a 32 kb region between the IRI1 and SPO7 genes.";
 CC RT genome 36:32-42(1993).
 CC RN [2]
 CC RP CHARACTERIZATION.
 CC RC MEDLINE=20408929; PubMed=10827169;
 CC RA Vickers M.F., Yao S.Y., Baldwin S.A., Young J.D., Cass C.E.;
 CC "Nucleoside transporter proteins of Saccharomyces cerevisiae.
 CC Demonstration of a transporter (FUT1) with high uridine selectivity
 CC in plasma membranes and a transporter (FUN26) with broad nucleoside
 CC selectivity in intracellular membranes.";
 CC RT J. Biol. Chem. 275:25931-25938(2000).
 CC CC -1- FUNCTION: HAS BROAD NUCLEOSIDE SELECTIVITY (URIDINE, ADENOSINE AND
 CC CYTIDINE) AND MOST LIKELY FUNCTIONS TO TRANSPORT NUCLEOSIDES
 CC ACROSS INTRACELLULAR MEMBRANES.
 CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC

CC -1- SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS.
 CC -----
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 CC or send an email to license@lsb-sib.ch).
 CC CC -----
 CC CC EMBL: L05146: AAC04935.1: -
 CC DR PIR: S36712: S36712.
 CC DR SGD: S0000020: FUN26.
 CC DR InterPro: IPR002259: DER/eqnu.transp.
 CC DR Pfam: PF01733: Nucleoside_tranp.1.
 CC DR ProDom: PD005103: DER/eqnu.transp.1.
 CC DR TIGRfams: TIGR00939: 2a57: 1.
 CC KW Transmembrane; Transport.
 CC FT TRANSMEM 76 96 POTENTIAL.
 CC FT TRANSMEM 116 136 POTENTIAL.
 CC FT TRANSMEM 151 171 POTENTIAL.
 CC FT TRANSMEM 174 194 POTENTIAL.
 CC FT TRANSMEM 214 234 POTENTIAL.
 CC FT TRANSMEM 243 263 POTENTIAL.
 CC FT TRANSMEM 344 364 POTENTIAL.
 CC FT TRANSMEM 367 387 POTENTIAL.
 CC FT TRANSMEM 411 431 POTENTIAL.
 CC FT TRANSMEM 446 466 POTENTIAL.
 CC FT TRANSMEM 492 512 POTENTIAL.
 CC SQ SEQUENCE 517 AA: 58317 MW: 43C92A3B9A3D8D50 CRC64;
 CC
 CC Query Match 11.5%: Score 96; DB 1; Length 517;
 CC Best Local Similarity 25.2%: Pred. No. 0.26;
 CC Matches 40; Conservative 30; Mismatches 71; Indels 18; Gaps 5;
 CC
 CC QY 16 VCIILNSHFLTEAGIHVFLIGCFSGAGLPKTEANVNVISDLKRIEDLIQSMHIDATY 75
 CC 343 YVLSIFFTFVTLVPEVPAASATVYTGIPLSNKOYPILEFTLMNDGLVGRVIAQMPMR 402
 CC 76 ESDVHPS-----CKVTAMKCFLELOVLSLGGASIHDPVENLLIANNLS----- 123
 CC DB 403 DKEFTPRKTFYISLRYAAIPFLMFTAITSSSGDEHNGSV--IVDLICYMLDPLRGV 460
 CC QY 124 SNGNV-TESGKCECELEEKKEFLDSEFVHI VDMFTINS 161
 CC 461 TNGHVISMSEFMKPELDLNDDEKKAAGGFNTI---FVST 496
 CC DB
 CC RESULT 11
 CC TRZA_RHOCO STANDARD; PRT: 476 AA.
 CC ID TRZA_RHOCO
 CC AC Q52725;
 CC DT 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE S-triazine hydrolase (EC 3.8.1.-) (N-ethylammelane chlorohydrolase).
 CC GN trza.
 CC OS Rhodococcus corallinus.
 CC OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 CC OC Actinomycetales; Corynebacterineae; Gordoniaceae; Gordonia.
 CC OK NCBI_TaxID=36822;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 CC RC STRAIN=NRRL 1544R;
 CC RA MEDLINE=96011356; PubMed=7592318;
 CC RA Shao Z.O., Seftens W., Mulhry W., Bekki R.M.;
 CC "Cloning and expression of the s-triazine hydrolase gene (trza) from
 CC Rhodococcus corallinus and development of Rhodococcus recombinant
 CC strains capable of dealkylating and dechlorinating the herbicide
 CC atrazine.";
 CC RT J. Bacteriol. 177:5748-5755(1995).
 CC CC -1- FUNCTION: HYDROLYTIC DEAMINATION OF THE S-TRIAZINE SUBSTRATE
 CC MELAMINE.
 CC

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CC CC -1- PATHWAY: Melamine degradation pathway; first step.
CC CC -1- SIMILARITY: BELONGS TO THE ATZ/TRZ FAMILY.
CC CC -----
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CC CC -----
DR EMBL: L16534; AAA90931.1; -
DR InterPro: IPR002604; ATZ_TRZ.
DR Pfam: PF01685; ATZ_TRZ; 1.
DR Hydrolase.
DR INTIMET 0
DR SEQUENCE 476 AA; 50727 MW; 64D953DB2E92C73E CRC64;

Query Match
Best Local Similarity 9.9%; Score 82.5; DB 1; Length 476;
Matches 26; Conservative 22; Mismatches 41; Indels 21; Gaps 3;

QY 40 SAGLPTKTNW---VNIISLKKIEDLIQSMHIDATLYTESDVHPSCKVTPAKCELLEQ 96
DB 320 TVGIGTDANCSVDNISDMKVALIHRARHASTITPFKITEATTIDCARCIGMAQD 379
QY 97 VLSLESGDAS-----IHDTVENLILAN---NSLSSNGNV 128
DB 380 ICSLEGGKRAADIITLDRIHAQTTPAHDIATIVQAGNVADVLVNGSV 429

RESULT 12
REBL_KLUA STANDARD; PRT; 595 AA.
AC 005950;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-binding protein REB1 (OBP).
GN REB1.
OS Kluyveromyces fragilis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93140755; PubMed=8423784;
RA Morrow B.E., Jr O., Warner J.R.;
RT "A bipartite DNA-binding domain in yeast Reb1p.";
RL Mol. Cell. Biol. 13:1173-1182(1993).
CC -1- FUNCTION: DNA-BINDING PROTEIN THAT RECOGNIZES SITES WITHIN BOTH
CC THE ENHANCER AND THE PROMOTER OF RNA TRANSCRIPTION. AS WELL AS
CC UPSTREAM OF MANY GENES TRANSCRIBED BY RNA POLYMERASE II. IT IS
CC ESSENTIAL FOR CELL GROWTH. MAY STIMULATE OR INHIBIT TRANSCRIPTION,
CC SPECIFICALLY RECOGNIZE THE SEQUENCE 5'-CGGGTA-3' OR 5'-CGGGTTR-3'
CC (WHERE R IS ANY PURINE) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
CC CC -----
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CC CC -----
DR EMBL: L03789; AAA61343.1; -
DR PIR: A48077; A48077.
DR HSSP: P06876; 1MBG.
DR TRANSFAC: T01245; -
DR InterPro: IPR001005; MYB_DNA_binding.
DR Pfam: PF00249; myb_DNA-binding; 3.

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DR SMART: SM00395; SANT; 4.
DR PROSITE: PS00037; MYB_1; 2.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS00090; MYB_3; 2.
KW Nuclear protein; DNA-binding; Transcription regulation; Repeat;
KW Phosphorylation.
FT DNA_BIND 337 MYB 1.
FT DNA_BIND 385 MYB 2.
FT SEQUENCE 595 AA; 68050 MW; 6A8533ACB3AF8162 CRC64;

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Query Match
Best Local Similarity 9.8%; Score 81.5; DB 1; Length 595;
Matches 28; Conservative 23; Mismatches 52; Indels 9; Gaps 2;

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QY 44 PRTFANWVNIISLKKIEDLIQSMHIDATLYTESDVHPSCKVTPAKCELLEQYTSLESG 103
DB 183 PKRKESEERSYDGLSNIDHDVDSVSGSIPSOVRLKTAAYLP-----KVLSSDSH 234
QY 104 DASIHDTVENLILANSSLSNGN-VTESGCKEPELEENIKRPLDSFVHI 154
DB 235 NDDQGDVSNLIDFAAKASHIINPATQSNKRSFDESEEALEQPIKEYORI 286

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RESULT 13
TRPA_BUCSC STANDARD; PRT; 269 AA.
AC 044604;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tryptophan synthase alpha chain (EC 4.2.1.20).
GN TRPA.
OS Buchnera aphidicola (subsp. Schlechtendalia chinensis).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95261545; PubMed=7742976;
RA Lai C.-Y., Baumann P., Moran N.A.;
RT "Genetics of the tryptophan biosynthetic pathway of the prokaryotic
RT endosymbiont (Buchnera) of the aphid Schlechtendalia chinensis.";
RL Insect Mol. Biol. 4:47-59(1995).
CC -1- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ADOL CLEAVAGE
CC OF INDOLGYCEROL PHOSPHATE TO INDOL AND GLYCERALDEHYDE 3-
CC PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate + H(2)O.
CC -1- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (by
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC CC -----
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CC CC -----
DR EMBL: U09185; AAA92797.1; -
DR HSSP: P00929; 2MSY.
DR InterPro: IPR03009; FMN enzyme.
DR InterPro: IPR002028; trp-synthaseA.
DR Pfam: PF00290; trp-syntA; 1.
DR PRODOM: PD001535; trp-synthaseA; 1.
DR TIGRfam: TIGR00262; trpA; 1.
DR PROSITE: PS00167; TRP_SYNTHASE_ALPHA; 1.
KW Tryptophan biosynthesis; Lyase.
SQ SEQUENCE 269 AA; 30301 MW; 7879A03A5C7A50AC CRC64;

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Query Match
Best Local Similarity 9.7%; Score 81; DB 1; Length 269;
Matches 25; Conservative 23; Mismatches 52; Indels 9; Gaps 2;

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Matches 40; Conservative 23; Mismatches 50; Indels 44; Gaps 7;

QY 3 ISKPHLRIS-IOCYLC-----LLNSHFLTEAGIHVFLIGCSAG-42
 Db 64 IOKAHLRAFSKKNVYICFEMLOKIRKXYTIPIGLLIYANLIFEGINNYLKCNVGI 123
 QY 43 -----LPKTEANWVVISDLK--IEDLQSHIDATLYTESDHPSCVYAMKCPFL 93
 Db 124 DSVILLADIPVEEN-----DFRKAIANNISSVFCP-----HDKKNVTKRISLY 169
 QY 94 ELQVLSGDSASIHDTVENLIILANSLSSNGVTE 130
 Db 170 STGYIYLLS-RSGVGTGDKKIIVPSLNLKMKKITE 205

RESULT 14
 RINT_RAT STANDARD; PRT: 456 AA.
 AC P29315;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease inhibitor.
 GN RNM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RA MEDLINE=92162755; PubMed=1536887;
 RX Kawanomoto M., Motojima K., Sasaki M., Hattori H., Goto S.;
 "cDNA cloning and sequence of rat ribonuclease inhibitor, and tissue
 distribution of the mRNA";
 RT Biochem. Biophys. Acta 1129:335-338(1992).
 RL Biochim. Biophys. Acta 1129:335-338(1992).
 CC -1- FUNCTION: INHIBITOR OF PANCREATIC RASP AND ANGIOENIN. MAY ALSO
 CC FUNCTION IN THE MODULATION OF CELLULAR ACTIVITIES.
 CC -1- SUBUNIT: FORMS A TIGHT ONE-TO-ONE COMPLEX WITH THE RASP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: BRAIN, HEART, LUNG, LIVER, SPLEEN, TESTES AND
 CC KIDNEY; HIGHEST IN THE LUNG AND LOWEST IN THE HEART.
 CC -1- SIMILARITY: CONTAINS 15 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 DR EMBL: X62528; CAA4388.1; -
 DR FTR: S20597; S20597.
 DR HSSP: P10775; 2BNH.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003590; LRR_Rninh.
 DR InterPro: IPR003592; LRR_out.
 DR Pfam: PF00560; LRR_3.
 DR SMART: SM00370; LRR_12.
 DR SMART: SM00368; LRR_R1; 1.
 DR Repeat, Leucine-rich repeat.
 KW Repeat, Leucine-rich repeat.
 FT REPEAT 15 43 LRR A1.
 FT REPEAT 44 71 LRR B1.
 FT REPEAT 72 100 LRR A2.
 FT REPEAT 101 128 LRR B2.
 FT REPEAT 129 157 LRR A3.
 FT REPEAT 158 185 LRR B3.
 FT REPEAT 186 214 LRR A4.
 FT REPEAT 215 242 LRR B4.
 FT REPEAT 243 271 LRR A5.
 FT REPEAT 272 299 LRR B5.
 FT REPEAT 300 328 LRR A6.

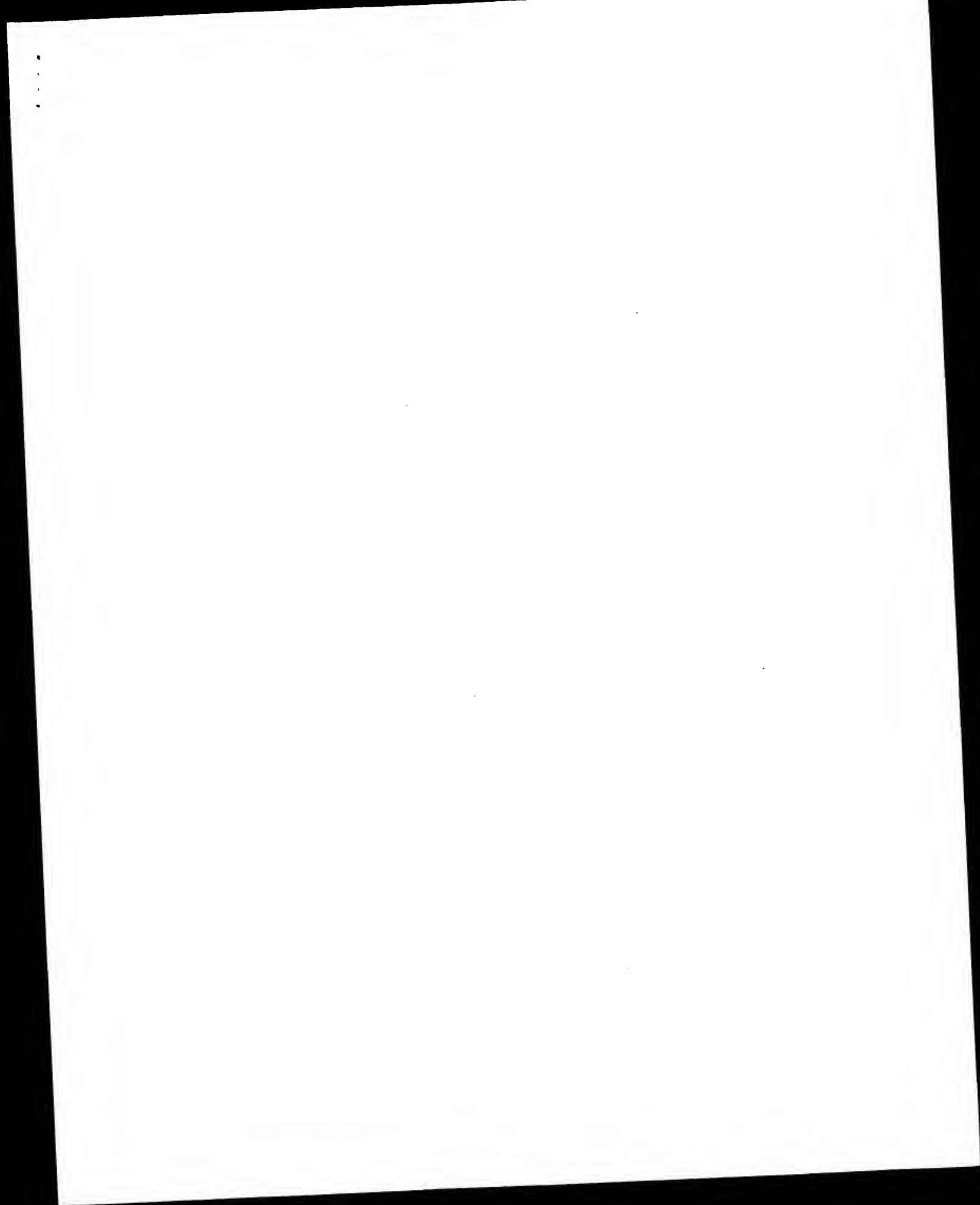
FT REPEAT 329 356 LRR B6.
 FT REPEAT 357 385 LRR A7.
 FT REPEAT 386 413 LRR B7.
 FT REPEAT 414 442 LRR A8.
 SQ SEQUENCE 456 AA; 49905 MW; 8518E5B1F09E5998 CRC64;

Query Match 9.5%; Score 79; DB 1; Length 456;
 Best Local Similarity 26.1%; Pred. No. 7.6;
 Matches 35; Conservative 26; Mismatches 51; Indels 26; Gaps 5;

QY 19 LLNSHFLTEAGIHVFLIGCSAGIIPKTEANWVVISDLKTEEDLQSHIDATLYTESD 78
 Db 170 LVLSNNDHFENAGIHTLCQG-----IKDSACQSLKLENCGITSAN 210
 QY 79 VHRSCGYAMKCFLELOVYLSLSDGASIHDTVENLIILANSLSS-----NGVTEGCK 134
 Db 211 CKDLDDVYASASLQELDLSGNKLGNGIALCSGL-LTPSCLRLTLMDCDVYAECK 269
 QY 135 E-CELEBK-NIKE 146
 Db 270 DICRYLRAKQSLKE 283

RESULT 15
 HCYG_SEPOF STANDARD; PRT: 560 AA.
 AC P56826;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Haemocyanin, units G and H (Fragments).
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidae; Sepioidae;
 OC Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP SEQUENCE OF 20-436 AND 446-560 FROM N.A.
 RA Declercq L., Witters R., Preaux G.;
 "Partial sequence determination of Sepia officinalis haemocyanin
 via cDNA";
 RT (in) Preaux G., Lontie R. (eds.);
 RL Invertebrate Dioxigen Carriers, pp.131-134, Leuven University Press,
 RL Leuven (1990).
 RN [2]
 RP PARTIAL SEQUENCE (H SUBUNIT).
 RA Vanderzande M., Gielens C., Preaux G.;
 "Isolation of functional units g and h from the haemocyanin of
 Sepia officinalis and partial amino-acid sequence of functional
 unit h";
 RT (in) Preaux G., Lontie R. (eds.);
 RL Invertebrate Dioxigen Carriers, pp.125-129, Leuven University Press,
 RL Leuven (1990).
 RN [3]
 RP SEQUENCE OF 1-19 AND 230-249, AND THIOETHER BOND.
 RX MEDLINE=98000289; PubMed=9342242;
 RA Gielens C., de Geest N., Xin X.-Q., Devreese B., van Beeumen J.,
 RA Preaux G.;
 "Evidence for a cysteine-histidine thioether bridge in functional
 units of molluscan haemocyanins and location of the disulfide bridges
 in functional units d and g of the beta-c-haemocyanin of Helix
 pomatia";
 RT Eur. J. Biochem. 248:879-886(1997).
 RL Funct. J. Biochem. 248:879-886(1997).
 CC -1- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
 CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
 CC ARTHROPODS.
 CC -1- COPACOR: CONTAINS TWO COPPER ATOMS PER FUNCTIONAL UNIT.
 CC -1- SUBUNIT: DECAmers OF LARGE IDENTICAL SUBUNITS (390 kDa), EACH
 CC CONTAINING 8 GLOBULAR OXYGEN-BINDING FUNCTIONAL UNITS.
 CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
 CC SUBFAMILY.
 DR InterPro: IPR002227; Tyrosinase.
 DR PRINTS: PR00092; TYROSINASE.
 DR PROSITE: PS00497; TYROSINASE_1; 1.

Search completed: February 20, 2003, 16:29:04
Job time : 18.5 secs



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OM protein - protein search, using sw model

Run on: February 20, 2003, 16:27:07 : Search time 61.5 Seconds

(without alignments)
542.758 Million cell updates/sec

Title: US-09-855-313A-2
Perfect score: 835
Sequence: 1 MRISKPHLRISIOCYCLD.....NIKEFLDSFVHIVDMFNTS 162

Scoring table: BIOSM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP virus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	63.8	128	6	Q8SPY0
2	247	29.6	187	13	Q9DEV5
3	238	28.5	187	13	Q9W756
4	114.5	13.7	143	13	Q42286
5	112.5	13.5	143	13	Q73883
6	111.5	13.4	143	13	Q73883
7	110.5	13.2	143	13	Q91AC7
8	109.5	13.1	143	13	Q42396
9	101.5	12.2	135	13	Q9PDM9
10	97.5	11.7	433	16	Q9ZGE7
11	94.5	11.3	162	4	Q9HBP4
12	92	11.0	382	16	Q8XN89
13	89	10.7	167	16	Q8XPC3
14	88.5	10.6	624	10	Q9ATD8
15	87.5	10.5	497	8	Q8W9S7
16	86.5	10.4	500	12	Q9YW85

17	85.5	10.2	855	5	Q02497	002497 drosophila
18	85	10.2	510	8	Q37631	037631 prototheca
19	84	10.1	167	2	Q46295	046295 clostridium
20	84	10.1	319	16	Q9P1B4	09P1B4 campylobact
21	84	10.1	796	10	Q8YV35	08YV35 zea mays (m
22	82.5	9.9	1249	16	Q9T0B6	09T0B6 arabidopsis
23	82.5	9.9	1553	10	Q8REU9	08REU9 fusobacteri
24	82.5	9.9	1553	10	Q8S479	08S479 zea mays (m
25	82	9.8	1794	10	Q8YV37	08YV37 zea mays (m
26	82	9.8	1794	10	Q8YV37	08YV37 zea mays (m
27	81.5	9.8	489	15	Q71154	071154 anabaena sp
28	81.5	9.8	589	6	Q95JZ9	095JZ9 human immun
29	81.5	9.8	642	5	Q21687	021687 macaca fasc
30	81.5	9.8	871	15	Q91K14	091K14 human immun
31	81.5	9.8	871	15	Q91K13	091K13 human immun
32	81.5	9.8	871	15	Q91K12	091K12 human immun
33	81	9.7	882	15	Q90024	090024 human immun
34	80.5	9.6	644	5	Q901V4	0901V4 caenorhabdi
35	80.5	9.6	922	5	Q16199	016199 caenorhabdi
36	80.5	9.6	1817	10	Q9M078	09M078 arabidopsis
37	80	9.6	366	16	Q8RCX4	08RCX4 thermococci
38	79.5	9.5	581	10	Q92SX2	092SX2 zea mays (m
39	79.5	9.5	364	16	Q9K828	09K828 bacillus ha
40	79.5	9.5	678	5	Q61493	061493 drosophila
41	79	9.5	308	2	Q9AJA7	09AJA7 shewanella
42	78.5	9.4	267	10	Q9FY96	09FY96 arabidopsis
43	78.5	9.4	684	2	Q65990	065990 clostridium
44	78.5	9.4	684	16	Q97MN8	097MN8 clostridium
45	78.5	9.4	689	5	Q97258	097258 plasmodium

ALIGNMENTS

RESULT 1
ID Q8SPY0 PRELIMINARY: PRT; 128 AA.
AC Q8SPY0:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Interleukin 15 (Fragment).
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SOURCE FROM N.A.
RA Xiang Z., Byrne K.M., Michal J.;
RT "Cytokine expression in muscle satellite cells of canine";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF479882; AAL87133.1; -
FT NON_TER
FT 128
SQ SEQUENCE 128 AA: 14192 MW: FC6BC2C2E1765934 CRC64;

Query Match
Best Local Similarity 63.8%; Score 533; DB 6; Length 128;
Matches 102; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY	1	MRISKPHLRISIOCYCLD.....NIKEFLDSFVHIVDMFNTS 162	0
DB	1	MRISKPHLRISIOCYCLD.....NIKEFLDSFVHIVDMFNTS 162	0
QY	61	EDLIOSMIDATLTYESVHPSCKVYAMKCFLEQLVISESDASIHDTVENTLITANN 120	0
DB	61	DNLIQCHMDTTLTYESVHPSCKVYAMKCFLEQLVISESDASIHDTVENTLITANN 120	0
QY	121	SLSSNGV 128	0
DB	121	DLSSKNI 128	0

RESULT 2

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Q9DEV5 ID Q9DEV5 PRELIMINARY: PRT: 187 AA.
AC Q9DEV5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Interleukin 15.
GN IL-15.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Stepaniak J.A., Kolodnick J.E., Hu W., Sundick R.S.;
RT "Chicken Interleukin 15 precursor, allelic variant.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005476; AAC02253.1;
DR InterPro; IPR003443; Interleukin_15.
DR Pfam; PF02372; IL15; 1.
SQ SEQUENCE 187 AA; 21879 MW; B701CFC07431B658 CRC64;

Query Match 29.6%; Score 247; DB 13; Length 187;
Best Local Similarity 39.0%; Pred. No. 1.3e-10; Indels 36; Gaps 9;
Matches 67; Conservative 22; Mismatches 47;

QY 5 KPHRSISICCYCLLNHFL---TEAGIHVFLGFSAGLPRTEAN---WNVISDL 57
DB 22 KTHVSTICDLYOLXLLNHFCLLNKKTGLTFPL---CAVPTETANKKWSVDLXL 78
QY 58 KRIEDLIOSMIDATLYTESDVHP-SCKVAMKCFLELOVLSLESGDASII---HDVYEN 113
DB 79 ELIK---TSEDIDVSLTYANTYEDIECEPEVMKCFLEKAVILHEGCKKCSRKHD-VVN 134
QY 114 LLIILANNSLSNGN-----VTESGCKCEDELEKNIKEFLDSFVHI 155
DB 135 IL-----KGNARPAATYOLNSTSKKCEKEVEEKNFTETIOSFVKVI 178

RESULT 3
Q9W756 ID Q9W756 PRELIMINARY: PRT: 187 AA.
AC Q9W756;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
DE Interleukin-15 precursor (Interleukin 15 precursor).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCW; TISSUE=LIVER;
RA Burnside J., Sofer L.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SC; TISSUE=LIVER;
RA Choi K.D., Lillehoj H.S., Burnside J.;
RT "Gallus gallus mRNA for IL-15 precursor.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152927; AAD38392.1;
DR EMBL; AF139097; AAF61446.1;
DR InterPro; IPR003443; Interleukin_15.
DR Pfam; PF02372; IL15; 1.
SQ SEQUENCE 187 AA; 21964 MW; 470601BFF8837095 CRC64;

Query Match 28.5%; Score 238; DB 13; Length 187;
Best Local Similarity 37.6%; Pred. No. 1e-15;

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Matches 65; Conservative 23; Mismatches 47; Indels 38; Gaps 9;

QY 5 KPHRSISICCYCLLNHFL---TEAGIHVFLGFSAGLPRTEAN---WNVISDL 57
DB 22 KTHVSTICDLYOLXLLNHFCLLNKKTGLTFPL---CAVPTETANKKWSVDLXL 78
QY 58 KRIEDLIOSMIDATLYTESDVHP-SCKVAMKCFLELOVLSLESGDASII---HDVYEN 112
DB 79 ELIK---TSEDIDVSLTYANTYEDIECEPEVMKCFLEKAVILHEGCKKCSRKHDV-- 132
QY 113 LLIILANNSLSNGN-----VTESGCKCEDELEKNIKEFLDSFVHI 155
DB 133 -----RNIMKNCNARPAATYOLNSTAKKCEKEVEEKNFTETIOSFVKVI 178

RESULT 4
Q42288 ID Q42288 PRELIMINARY: PRT: 143 AA.
AC Q42288;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Interleukin-2 precursor.
GN IL2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSTREL LECHORN; TISSUE=SPLEEN;
RA Huchard R.S., Tyckowski J.K., Poston R.M., Hester J.B.,
RT "Gallus gallus mRNA for IL-2 precursor.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035563; AAB87502.1;
DR InterPro; IPR000779; Interleukin-2.
DR InterPro; IPR003443; Interleukin_15.
DR Pfam; PF02372; IL15; 1.
DR SMART; SM00189; IL2; 1.
KW signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 143 INTERLEUKIN-2.
FT VARIANT 28 28 E->A.
FT VARIANT 30 30 W->R.
FT VARIANT 32 32 T->P.
SQ SEQUENCE 143 AA; 16429 MW; 7DCDEACBD48F5AC CRC64;

Query Match 13.7%; Score 114.5; DB 13; Length 143;
Best Local Similarity 26.2%; Pred. No. 0.0013; Indels 25; Gaps 7;
Matches 37; Conservative 25; Mismatches 50;

QY 33 VFLTGFSAGLPRTEA-----NW---VNVISDLKRIEDLIOSMIDATLYTESDVHP 81
DB 5 VFLPGISVAMMTATAYGASLSEKKTLOTILIKLEILNKNKHDE-LYPTETO- 61
QY 82 SKCVAMKCFLELOVLSLESGASTHOT-VENLLILANNSLSN-----GNVTESGCK 134
DB 62 ECTGQULOCYGLDEVVTLKKTED---DTEIKERVTAIONIEKNLKSITGLNTGSECK 117
QY 135 ECELEKNIKEFLDSFVHI 155
DB 118 ICEANKKKKFPDFLHLELNFV 138

RESULT 5
Q73883 ID Q73883 PRELIMINARY: PRT: 143 AA.
AC Q73883;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)

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DE IL-2 precursor (Interleukin-2).
GN INTERLEUKIN-2 OR IL2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaiser P., Mariani P.;
RL Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Choi K.D., Lillehoj H.S., Song K.D., Han J.Y.;
RC STRAIN=SC;
RA "Molecular and Functional Studies of Chicken IL-15 Which Promotes the
RT Growth of gamma/delta TCR T Lymphocytes: Phenotypic and Functional
RL Characterization of IL-15 dependent gamma/delta T cells."
RN [3]
RP Dev. Comp. Immunol. 0:0-0(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen.
RA Yu L., Li J.R., Huang Y.W., Meng S.S.;
RT "Cloning and sequence analysis of a Chinese local chicken IL-2 gene."
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ224516; CAI12025.1; -
DR EMBL: AF017645; AAC96064.1; -
DR EMBL: AF029588; AAK37773.1; -
DR InterPro: IPR000779; Interleukin-2.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
DR SMART: SM00189; IL2; 1.
KW signal.
FT CHAIN 1 22 POTENTIAL.
SQ SEQUENCE 143 AA: 16337 MW: 163697545466 CRC64;

Query Match 13.5%; Score 112.5; DB 13; Length 143;
Best Local Similarity 25.5%; Pred. No. 0.002;
Matches 36; Conservative 26; Mismatches 54; Indels 25; Gaps 6;

QY 33 VFLICFSAGLPTKTEAMWVN-----VISDLKRIEDLIQSMHIDATLYTESDVHP 81
DB 5 VLIIFCSVALMTTAYGASLSPEKLEILPALIKDLIEESKNNIHV--VLTYPNEI-K 61
QY 82 SCKVYAMKCFLELYVLSLSDASIHDT-VENLLILANNSLSSNGVTESSGCK 134
DB 62 ECTOQTLCYCLEEVMKKETED---DFEIKKEFVTAIONIEKNLSLGLNHTGSECK 117
QY 135 ECELEKNIKKEFLDSFVHIY 155
DB 118 ICEANNNKKRPDLHLHTNFY 138

RESULT 6
Q9PT81 PRELIMINARY: PRT: 143 AA.
AC Q9PT81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-2 precursor.
GN IL2.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20177011; PubMed=10714551;
RA Lawson S.A., Rothwell L., Kaiser P.;
RT "Turkey and chicken interleukin-2 cross-react in in vitro
proliferation assays despite limited amino acid sequence identity."

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RL J. Interferon Cytokine Res. 20:161-170(2000).
DR EMBL: AJ007463; CAB65230.1; -
DR InterPro: IPR000779; Interleukin-2.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
DR SMART: SM00189; IL2; 1.
KW signal.
FT CHAIN 1 20 POTENTIAL.
SQ SEQUENCE 143 AA: 16511 MW: 165088749550CB CRC64;

Query Match 13.4%; Score 111.5; DB 13; Length 143;
Best Local Similarity 24.8%; Pred. No. 0.0025;
Matches 34; Conservative 28; Mismatches 58; Indels 17; Gaps 5;

QY 33 VFLICFSAGLPTKTEAMWVN-----VISDLKRIEDLIQSMHIDATLYTESDVHP 81
DB 5 VLIIFCSVALMTTAYGASLSPEKLEILPALIKDLIEESKNNIHV--VLTYPNEI-K 61
QY 82 SCKVYAMKCFLELYVLSLSDASIHDTVENLLILANNSLSSNGVTESSG--CKECE 138
DB 62 ECTOQTLCYCLEEVMKKETEDPEIKKEFNALONIKRNLRLKDLSPGGECKICEA 121
QY 139 LEEKNIKKEFLDSFVHIY 155
DB 122 NDKKNWPDLOQLTNFY 138

RESULT 7
Q9IAC7 PRELIMINARY: PRT: 143 AA.
AC Q9IAC7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-2.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA Romero C.H., Cai X.Z.;
RT "Turkey interleukin-2 gene."
RL Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF209705; AAF35206.1; -
DR InterPro: IPR000779; Interleukin-2.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
DR SMART: SM00189; IL2; 1.
SQ SEQUENCE 143 AA: 16442 MW: 164409593488B22B CRC64;

Query Match 13.2%; Score 110.5; DB 13; Length 143;
Best Local Similarity 24.1%; Pred. No. 0.0031;
Matches 33; Conservative 30; Mismatches 57; Indels 17; Gaps 5;

QY 33 VFLICFSAGLPTKTEAMWVN-----VISDLKRIEDLIQSMHIDATLYTESDVHP 81
DB 5 VLIIFCSVALMTTAYGASLSPEKLEILPALIKDLIEESKNNIHV--VLTYPNEI-K 61
QY 82 SCKVYAMKCFLELYVLSLSDASIHDTVENLLILANNSLSSNGVTESSG--CKECE 138
DB 62 ECTOQTLCYCLEEVMKKETEDPEIKKEFNALONIKRNLRLKDLSPGGECKICEA 121
QY 139 LEEKNIKKEFLDSFVHIY 155
DB 122 NDKKNWPDLOQLTNFL 138

RESULT 8
O42396 PRELIMINARY: PRT: 143 AA.
AC O42396;

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DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin-2.
GN IL-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OBES; G11-Dixon C.;
RA Sundick R.S.; G11-Dixon C.;
RT "A cloned chicken lymphokine homologous to both mammalian IL-2 and IL-
RT 15."
RL J. Immunol. 0:0-0(1997).
DR EMBL: AF000631; AAB63150.1;
DR InterPro: IPR000779; Interleukin-2.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
DR SMART: SM00189; IL2; 1.
DR SMART: SM00189; IL2; 1.
SQ SEQUENCE 143 AA; 16307 MW; B9B1E997A54935F CRC64;

Query Match 13.1%; Score 109.5; DB 13; Length 143;
Best Local Similarity 25.5%; Pred. No. 0.004;
Matches 36; Conservative 25; Mismatches 55; Indels 25; Gaps 6;

OY 33 VFLIGESAGLKPTEANVNV-----VISPLKIEPLIQSMHIDATLYESDVHP 81
DB 5 VLLIGESAVATMTMTAYASASSAKKRPQTLTKLLELEINKKHLF-LYPTETQ- 61
OY 82 SCVYAMKCFLELOVLSGDSADHD-VENLLIANNLSN-----GNVTEGCK 134
DB 62 ECTQTLQCLVGVLTETKEDD---DTEIKKEFVAIONIEKNLSLMLGHNHSGCK 117
OY 135 ECELEKKEKKEPDSFVHV 155
DB 118 ICEANKKKPPDFLHETNFV 138

RESULT 9
O9DDN9 PRELIMINARY; PRT; 135 AA.
AC O9DDN9:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Interleukin-2 (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEN;
RA Hu W.; Koldosick J.E.; Stepaniak J.A.; Sundick R.S.;
RT "Turkey Interleukin-2."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF08569; AAG35189.1;
DR InterPro: IPR000779; Interleukin-2.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
DR SMART: SM00189; IL2; 1.
DR SMART: SM00189; IL2; 1.
FT NON_TER 1
SQ SEQUENCE 135 AA; 15460 MW; 326F88A3563D13E8 CRC64;

Query Match 12.2%; Score 101.5; DB 13; Length 135;
Best Local Similarity 23.5%; Pred. No. 0.023;
Matches 31; Conservative 29; Mismatches 55; Indels 17; Gaps 5;

OY 38 CFSAGLPTEANVNV-----VISDLKIEPLIQSMHIDATLYESDVHPGCKVT 86

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DB 2 CISVALMTTAYGASLSPKLEILPALIKPLEEESKNKIHV--VLYTPNEI-KECSQ 58
OY 87 AMKCFLELOVLSGCD-ASLHDTVENLLIANNLSNGNVNDSG--CKECELEKKN 143
DB 59 TLQCYLEEMVLEKEIDEPEIKNEFNALONIKNLHRLKGLSPGEGCKICEANDKN 118
OY 144 IKEPDSFVHV 155
DB 119 FDPFLQQLTNLL 130

RESULT 10
O92GE7 PRELIMINARY; PRT; 433 AA.
AC O92GE7:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical Protein RC1176.
GN RC1176.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."
RL Science 293:2093-2098(2001).
DR EMBL: AE008665; AL03714.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 433 AA; 48342 MW; 4934702460B02E6 CRC64;

Query Match 11.7%; Score 97.5; DB 16; Length 433;
Best Local Similarity 19.7%; Pred. No. 0.24;
Matches 37; Conservative 39; Mismatches 65; Indels 47; Gaps 8;

OY 10 SISLCYLCILLN-----SHFLTEAGIHV-----ILGCSAG--LPTEANV 51
DB 6 NINKEVMEPEFSENEIVSRISGNVSHLHKLSSTIFSSVSTVEGAKKGYIVDMQCNK 65
OY 52 NVISDLKIEDLIQSMHIDA-----TLTSDVHPGCKVTAMKCFLELOVLS 102
DB 66 NIEQSFESNDFSIHQECNGLNIPINNIFIDANNPH-----LLQGVTPHQN 117
OY 103 GDASIHDTVENLLIANNLSNGNVNDSG-----GCKECELEKKEKKEPDSFVHV 155
DB 118 GTAST--LSQLYKVMNDYIFSGNITETSGADFLGNECKYKEAMSALQNVNAYETLI 174
OY 156 --DMETNF 161
DB 175 PRESENT 182

RESULT 11
O9HBE4 PRELIMINARY; PRT; 162 AA.
AC O9HBE4:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin 21.
GN IL21.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20531754; PubMed=1081504;
 RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
 Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
 Burkhead S., Heipel M., Brandt C., Kulper J.L., Kramer J.,
 Conklin D., Presnell S.R., Berry J., Shioa F., Bort S., Hamby K.,
 Modli S., Clegg C., Moore M., Grant F., Lofton-Day C., Gilbert T.,
 Rayond F., Ching A., Tao L., Smith D., Webster P., Whitmore T.,
 Maurer M., Kausanskyy K., Holly R.D., Foster D.,
 "Interleukin 21 and its receptor are involved in NK cell expansion and
 regulation of lymphocyte function."
 RA Nature 408:57-63(2000).
 RL EMBL: AF254069; AAC29348.1;
 SO SEQUENCE 162 AA; 18652 MW; 54EFD4EBDAB97FE CRC64;

Query Match 11.3%; Score 94.5; DB 4; Length 162;
 Best Local Similarity 25.0%; Pred. No. 0.14;
 Matches 29; Conservative 23; Mismatches 49; Indels 15; Gaps 5;

OY 51 VNVISDLK-IEDLIQSMHIDATYTESDVHPSCKVYMKCELEQVLSGDSASIH 109
 DB 43 IDYDQAKNVNDLVEP-----LPAPEDVETNCMSAFSCF-----OKAQLSANTGNNE 93
 OY 110 TVENLIT--LANNLSNGNTES--GCKECEELEENIKKEFLDSFVHIYDFIN 160
 DB 94 RITVNSIKRLKRPPTVAGRHKRLTPSCDYERKPKPELEFRKSLQMKIH 149

RESULT 12

O8XN89 PRELIMINARY; PRT; 382 AA.
 AC O8XN89;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-JUN-2002 (TREMBlrel. 20, Last sequence update)
 DE Alcolol dehydrogenase.
 GN ABH OR CPE0049.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 RN NCBI_TaxID=1502;
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohlani K., Hirakawa H., Ohshima K., Yamashita A.,
 Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
 "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL: AP003186; BAB80155.1;
 DR InterPro: IPR001670; Fe-ADH.
 DR Pfam: PF00465; Fe-ADH.
 DR PROSITE: PS00913; ADH_IRON_1;
 DR PROSITE: PS00060; ADH_IRON_2;
 KW Complete proteome.
 SO SEQUENCE 382 AA; 40823 MW; 8030D0269P2E32 CRC64;

Query Match 11.0%; Score 92; DB 16; Length 382;
 Best Local Similarity 23.6%; Pred. No. 0.72;
 Matches 47; Conservative 29; Mismatches 63; Indels 60; Gaps 8;

OY 20 LNSFLTEGIVHIFLIGFSGLPKEANWVNSDLKIEDLIQSMHIDATYTESDV 79
 DB 12 LMGADCKADGQDVGELG-FKRLALITD--KVLGQIGIVKVTVDLDKKNLEFVAYDERKP 69
 OY 80 HPSCK-VTAKCFLELDQ--VISLESQDASHIDVENVLLILANN-----120
 DB 70 NPTVKNVNDGLALKEKCEQVLSL--GGSAHDAKAKIALANNGSETKQEGYDKSK 127
 OY 121 -SLSSNGNTESGCKECEL-----EKNIKEFL-----148
 DB 128 POLPMVGINTAGTGSSEMTLPALITDERHIMALVYKHLPTIIVANDPMLAMPSRL 187

OY 149 -----DSFVHIYDFINTS 162
 DB 188 AATGMALTHALEAVSVTS 206

RESULT 13

O8XPC3 PRELIMINARY; PRT; 167 AA.
 AC O8XPC3;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE Hypothetical protein CPE0042.
 GN CPE0042
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 RN NCBI_TaxID=1502;
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohlani K., Hirakawa H., Ohshima K., Yamashita A.,
 Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
 "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL: AP003185; BAB79748.1;
 KW Hypothetical protein; Complete
 SO SEQUENCE 167 AA; 18821 MW; AD25C70C57665B3A CRC64;

Query Match 10.7%; Score 89; DB 16; Length 167;
 Best Local Similarity 21.9%; Pred. No. 0.51;
 Matches 32; Conservative 28; Mismatches 50; Indels 36; Gaps 4;

OY 31 HVEFLGCFAGLPKTEANWVNSD-----LKTIEDLIQSMHIDATYTE 76
 DB 14 ISLFLVLCSTGS-----EKNTINIPLEKREESKDEDEYIDKISSTVMSVDSISKNM 69
 OY 77 SDVHPSCKV-----TAMKCELEQVLSGDSASIHVENVLLILANNLS 124
 DB 70 RIVSETEGKLNNTINIDQLERSNNFVKCLIEDLGKVPKFAVYNDIDINLAKKATSLA 129
 OY 125 NGVNTESGCKECEELEENIKKEFLDS 150
 DB 130 MKNSHD-----ETIKSNMAKIFVES 149

RESULT 14

O9ATD8 PRELIMINARY; PRT; 624 AA.
 AC O9ATD8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 GN GHDEL61.
 OS Gossypium hirsutum (upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Malvales; Malvaceae; Gossypium.
 RN NCBI_TaxID=3635;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ACALA MAXXA; TISSUE=DAY OF ANTHESIS OVULE;
 RA Matz E.C., Burr B.;
 RT "Cotton seed fibers are trichomes."
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF336279; AAK19612.1;
 DR HSSP: P36956; 1A89.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00010; HLH; 1.
 DR SMART: SM00353; HLH; 1.

Search completed: February 20, 2003, 16:31:15

Fri Feb 21 08:45:03 2003

us-09-855-313a-4.raj

Page 1

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 20, 2003, 16:27:07 ; Search time 33 Seconds
(without alignments)

654,139 Million cell updates/sec

Title:
US-09-855-313A-4

Perfect score:
833

Sequence:
1 MRISKPHLRISITOCYICLL.....NIKEFLQSFVHYVMEINTS 162

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:
908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:
908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing First 45 summaries

Database :

A-Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	833	100.0	162	16	AAAR3438
2	833	100.0	162	16	AAAR6927
3	833	100.0	162	17	AAAR6927
4	833	100.0	162	17	AAAR6927
5	833	100.0	162	17	AAAR6927
6	833	100.0	162	18	AAAR6927
7	833	100.0	162	18	AAAR6927
8	833	100.0	162	18	AAAR6927
9	833	100.0	162	19	AAAR6927
10	833	100.0	162	20	AAAR6927

11	833	100.0	162	21	AAAR6927
12	833	100.0	162	21	AAAR6927
13	833	100.0	162	21	AAAR6927
14	833	100.0	162	22	AAAR6927
15	833	100.0	162	22	AAAR6927
16	833	100.0	162	22	AAAR6927
17	833	100.0	162	22	AAAR6927
18	833	100.0	162	22	AAAR6927
19	833	100.0	162	22	AAAR6927
20	833	100.0	162	22	AAAR6927
21	833	100.0	162	22	AAAR6927
22	833	100.0	162	22	AAAR6927
23	833	100.0	162	22	AAAR6927
24	833	100.0	162	22	AAAR6927
25	833	100.0	162	22	AAAR6927
26	833	100.0	162	22	AAAR6927
27	833	100.0	162	22	AAAR6927
28	833	100.0	162	22	AAAR6927
29	833	100.0	162	22	AAAR6927
30	833	100.0	162	22	AAAR6927
31	833	100.0	162	22	AAAR6927
32	833	100.0	162	22	AAAR6927
33	833	100.0	162	22	AAAR6927
34	833	100.0	162	22	AAAR6927
35	833	100.0	162	22	AAAR6927
36	833	100.0	162	22	AAAR6927
37	833	100.0	162	22	AAAR6927
38	833	100.0	162	22	AAAR6927
39	833	100.0	162	22	AAAR6927
40	833	100.0	162	22	AAAR6927
41	833	100.0	162	22	AAAR6927
42	833	100.0	162	22	AAAR6927
43	833	100.0	162	22	AAAR6927
44	833	100.0	162	22	AAAR6927
45	833	100.0	162	22	AAAR6927

ALIGNMENTS

RESULT 1	AAAR3438	standard; Protein: 162 AA.
ID	AAAR3438	
AC	AAAR3438	
XX		
DT	02-FEB-1996	(first entry)
XX		
DE	Human interleukin-15 precursor.	
KW	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte.	
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	Peptide	1..48
FT		/label= leader
XX		
PN	W09527722-A.	
PD	19-OCT-1995.	
XX		
PR	06-APR-1994;	94WO-US03793.
XX		
PR	06-APR-1994;	94WO-US03793.
XX		
PA	(IMMUNEX CORP.	
XX		
PI	Anderson DM, Eisman JR, Fung V, Grabstein KH;	
XX	Rauch C;	
XX		
DR	WPI: 1995-37356/48.	
	N-PSDB: AAT00526.	

XX A simian species of IL-15 (sIL-15) was purified and its AA
CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,
CC AAT00524, AAT00525). Both the simian and the human orfs encode
CC a precursor polypeptide (AAR83436, AAR83437). The precursor
CC polypeptides each comprise a 48-AA leader sequence and a sequence
CC encoding mature simian or human IL-15 polypeptides. The active
CC simian and human IL-15 polypeptides are disclosed in AAR8309 &
CC AAR8330 respectively. The invention also comprises other mammalian
CC IL-15, including human IL-15, that hybridise to probes defined by
CC AAR83438. A plasmid contg. a recombinant clone of human IL-15
CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 65245.
CC The deposit was named 141-heRF. AAR83439 is a mammalian mature
CC IL-15 polypeptide. It is a generic sequence which encompasses both
CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.

XQ Sequence 162 AA:

```

QY      1 MRKSRPHLRISIDCYCLCLLNHSHEFLTEAGIHFEILGCSAGKRIEANNVN
Db      1 MRKSRPHLRISIDCYCLCLLNHSHEFLTEAGIHFEILGCSAGKRIEANNVN 60
QY      61 EDLIGSMHIDATITEDSDVHSPCKVTAKKCELEIYOISLESGBASIHDTVERILLANN
Db      61 EDLIGSMHIDATITEDSDVHSPCKVTAKKCELEIYOISLESGBASIHDTVERILLANN 120
QY      61 EDLIGSMHIDATITEDSDVHSPCKVTAKKCELEIYOISLESGBASIHDTVERILLANN
Db      61 EDLIGSMHIDATITEDSDVHSPCKVTAKKCELEIYOISLESGBASIHDTVERILLANN 120
QY      121 SLSSNGNWTESGCKCELELEKNIKRFFLOSIVHIVQMEINTS 162
Db      121 SLSSNGNWTESGCKCELELEKNIKRFFLOSIVHIVQMEINTS 162
QY      121 SLSSNGNWTESGCKCELELEKNIKRFFLOSIVHIVQMEINTS 162
Db      121 SLSSNGNWTESGCKCELELEKNIKRFFLOSIVHIVQMEINTS 162

```

XX	AAR66927;
AC	
XX	
DT	04-SEP-1995 (first entry)

XX	Interleukin-15; IL-15; hIL-15; T-cell growth factor
KW	antitumor; virucide.
KW	

AA	key	Location/Qualifiers
FH		148

```

11      /label= sig_peptide
12      49 162
13      FT

```

```

/label= mal_peptide
/note= "active human IL-15"

```

XX
DN
7A9402636-A-

XX
PD
28-DEC-1994

AA 18-APR-1994; 94ZA-0002636.
PF

PR 18-APR-1994; 94ZA-0002036

PA (IMMV) IMMUNEX CORE
 VY

PI Anderson DA
PI Rauch C;
XX
DR WPI: 1995-082473/11
DR N-PSDB: AAQ84584.
DR

PT New purified interleukin-15 - which induces a cell proliferation used for the treatment of tumours and viral

PT infection

PS Claim 24; Page 28-29; 4/6pp; encl. 10

xx [redacted] interleukin-15

CC A S1.13 probe was first used to screen a cDNA library generated from the marrow stromal cells. Clone

CC I41.hETF encoded human IL-15.

Sequence 162 AA; tooth 162

Query Match	100.00;		
Post Local Similarity	100.08;		
	Pred.	No. 2e-85;	
		0.	Indels
			Gaps
			0;

Matches 102; Conservation 60

0Y I
|||||
|||NSHETAGHYFLGCFSSAGLPKTEANWNVNISDLKI 6C

[illegible]

61 EDILOSMDATLTESDVHPSCKVTAMKCFLELOVISLESCDASIHDTVENLLIANN 120

121 SLSNNGVTESGCKECELEENIKELQSFVHIVQMETNTS 162

121 SSSNGVTESGCKECELEKNIKEFLÖSFVHIVÖM INJÖ 100

AAW09098 standard; protein; 162 AA.

XX
AC
AAW09098;

11-MAR-1997 (first entry)

Simian epithelium derived T cell factor

KM SETF; African green monkey; differentiation; gastrointestinal, lymphocyte; proliferation; differentiation; gastrointestina

XX KW HIV Infection, Human

05
XX

FT	Peptide	Label = leader
1	1	48

Protein	49..102 /label= mature_sETF
FT	

XX
DN
1155574138-A

XX
PD 12-NOV-1996

AA 08-MAR-1993; 93US-0031399.
PF

PR 22-FEB-1995; 95US-0393305
PR 22-FEB-1995; 93US-0031399

PR 22-APR-1994; 9405-0235000
VY

PA (IMMV) IMMONEA CO. XX
XX

PI Anderson
PI Rauch C;

:

DR WPI: 1996-517923/51.
 DR N-PSDB: AAT49455.
 XX
 PT New epithelium derived T cell factor - induces proliferation of T
 PT and B cells, stimulates destruction of tumour and virus-infected
 PT cells and protects against toxicity, partic. for treating intestinal
 PT disease and HIV infection
 XX
 PS Claim 1: Fig 1: 35pp; English.
 XX
 CC The simian ETP (epithelium derived T cell factor) was isolated from
 CC African green monkey CV1/EBNA cell conditioned medium. The N-
 CC terminal sequence of the purified ETP was determined and then PCR
 CC primers were designed based on the sequence information. A 92 bp
 CC fragment was amplified from CV1/EBNA DNA and was used as a probe to
 CC screen a CV1/EBNA cDNA library for the full-length ETP coding
 CC sequence. Mature ETP induces proliferation and/or differentiation
 CC of precursor or mature T cells and is useful for promoting long-term
 CC in vitro culture of T-lymphocytes and T-cell lines. It is used for
 CC treating gastrointestinal diseases including peptic ulcer, colitis and
 CC malignancy and for treating HIV infection.
 CC
 SQ Sequence 162 AA:
 Query Match
 Best Local Similarity 100.0%; Score 833; DB 17; Length 162;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MRISKPHRLSISIOCYCLILNSHFLTEAGIHVFLTCPSAGIPKTEANWNVISDLKTI 60
 DB 1 MRISKPHRLSISIOCYCLILNSHFLTEAGIHVFLTCPSAGIPKTEANWNVISDLKTI 60
 OY 61 EDLISGMHIDATLTESDVHPSCKVTAMKCFLELOVLSLESGDASHDVENLITLANN 120
 DB 61 EDLISGMHIDATLTESDVHPSCKVTAMKCFLELOVLSLESGDASHDVENLITLANN 120
 OY 121 SLSNGNVTEGCKECELEENKIKFLOSFFVHIVOMFINTS 162
 DB 121 SLSNGNVTEGCKECELEENKIKFLOSFFVHIVOMFINTS 162
 RESULT 4
 ID AAM07255 standard; Protein: 162 AA.
 AC AAM07255;
 XX
 DT 05-FEB-1997 (first entry)
 XX
 DE Human epithelium-derived T cell factor.
 XX
 KW Epithelium-derived T-cell factor; simian; human; culture; proliferation;
 KW epithelial cell; differentiation; T-lymphocyte; African green monkey;
 KW primer; PCR; polymerase chain reaction; amplification; probe.
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide 1..48 Location/Qualifiers
 FT /note= "signal peptide"
 FT Protein 49..162
 FT /note= "mature protein"
 XX
 PN US5552303-A.
 XX
 PD 03-SEP-1996.
 XX
 PF 08-MAR-1993; 93US-0031399.
 XX
 PR 08-MAR-1993; 93US-0031399.
 XX
 PA (IMMV) IMMUNEX CORP.

PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
 XX WPI: 1996-412063/41.
 DR N-PSDB: AAT42243.
 XX
 PT New isolated simian and human epithelium-derived T-cell factors -
 PT which stimulate the proliferation and/or differentiation of
 PT T-lymphocytes and T-cell lines
 XX
 PS Claim 21: Column 23-24; 22pp; English.
 XX
 CC This is the amino acid sequence of a human epithelium-derived T-cell
 CC factor (ETP). The gene was obtained using a 1.37 kb fragment of the
 CC corresp. African green monkey gene (AAT42242) as a probe to screen a
 CC cDNA library constructed from RNA derived from the IMTLH cell line. This
 CC cell line is derived by stable transformation of a human bone marrow
 CC stromal cell culture with pSV3neo. From a pool of about 1000 cDNA
 CC clones, one clone 141.HEP contained the gene. ETP is a protein of 15-17
 CC kD which is expressed by epithelial cells and stimulates proliferation
 CC and/or differentiation of precursor and/or mature T cells. The protein
 CC is therefore useful for promoting long term in vivo culture of
 CC T-lymphocytes and T-cell lines.
 CC
 SQ Sequence 162 AA:
 Query Match
 Best Local Similarity 100.0%; Score 833; DB 17; Length 162;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MRISKPHRLSISIOCYCLILNSHFLTEAGIHVFLTCPSAGIPKTEANWNVISDLKTI 60
 DB 1 MRISKPHRLSISIOCYCLILNSHFLTEAGIHVFLTCPSAGIPKTEANWNVISDLKTI 60
 OY 61 EDLISGMHIDATLTESDVHPSCKVTAMKCFLELOVLSLESGDASHDVENLITLANN 120
 DB 61 EDLISGMHIDATLTESDVHPSCKVTAMKCFLELOVLSLESGDASHDVENLITLANN 120
 OY 121 SLSNGNVTEGCKECELEENKIKFLOSFFVHIVOMFINTS 162
 DB 121 SLSNGNVTEGCKECELEENKIKFLOSFFVHIVOMFINTS 162
 RESULT 5
 ID AAR98527 standard; Protein: 162 AA.
 AC AAR98527;
 XX
 DT 17-NOV-1996 (first entry)
 XX
 DE Human interleukin-15.
 XX
 KW Interleukin-15; antagonist; mutein; graft versus host disease;
 KW allograft; T-cell growth factor.
 OS Homo sapiens.
 XX
 FH Key
 FH MISC-difference 56 Location/Qualifiers
 FT MISC-difference 156 /note= "preferred site for amino acid substn."
 FT MISC-difference 156 /note= "preferred site for amino acid substn."
 XX
 PN WO9626274-A1.
 XX
 PD 29-AUG-1996.
 XX
 PF 21-FEB-1996; 96WO-US02520.
 XX
 PR 22-FEB-1995; 95US-0392317.
 XX
 PA (IMMV) IMMUNEX CORP.

XX 28-NOV-1996.
 XX 07-MAY-1996; 96NO-US06423.
 XX 24-MAY-1995; 95US-0535733.
 XX (IMV) IMMUNEX CORP.
 XX Grabstein KH, Oulinn LS, Troutt AB;
 XX MPI: 1997-020939/02.
 XX N-PSDB: AAT56404.
 XX Muscle trophic compsn. contg. interleukin 15 - for treating, e.g.
 XX congestive heart failure, muscle wasting etc.
 XX Disclosure: Page 12; 22pp; English.
 XX This sequence is human Interleukin-15 (IL-15), a known T-cell growth
 XX factor that can support proliferation of an IL-2-dependent cell line,
 XX CTL-2. Compsn. contg. IL-15 to stimulate muscle growth, differentiation
 XX or hypertrophy are claimed. The stimulation of muscle growth is useful
 XX for treating atrophy, or wasting, in particular, skeletal and cardiac
 XX muscle atrophy. The compsn. further comprises a steroid, growth hormone
 XX and insulin-like growth factor. Congestive heart failure, growth hormone
 XX and diabetes-associated glucose-intolerance or dyslipidaemia,
 XX rhabdomyosarcoma and muscular dystrophy can all be treated by such
 XX compsns..

Sequence 162 AA:

Query Match 100.0%; Score 833; DB 18; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-85;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRISKPHRSTISIOCYCLLNNSHFLTEAGIHVFLIGCFSAQIPTEANWNVISDLKI 60
 DB 1 MRISKPHRSTISIOCYCLLNNSHFLTEAGIHVFLIGCFSAQIPTEANWNVISDLKI 60
 OY 61 EDIISMHIDATLTYESDVHPSCVTAMKCFLELOVISLESGDASHDTVENLITLANN 120
 DB 61 EDIISMHIDATLTYESDVHPSCVTAMKCFLELOVISLESGDASHDTVENLITLANN 120
 OY 121 SLSNGNVTESGCKECEELEEKNIKEFLQSFVHIVOMFNTS 162
 DB 121 SLSNGNVTESGCKECEELEEKNIKEFLQSFVHIVOMFNTS 162

RESULT 8

AAM53878
 ID AAM53878 standard; Protein: 162 AA.

XX AAM53878;

XX 13-JUL-1998 (first entry)

XX Human interleukin-15.

XX Human; interleukin-15; IL-15; T cell; B cell; proliferation; vaccine;
 XX cytokine; growth factor.

XX Homo sapiens.

XX US5747024-A.

XX 05-MAY-1998.

XX 19-JUN-1995; 95US-0504042.

XX 19-JUL-1995; 95US-0504042.

XX 08-MAR-1993; 93US-0031399.
 XX 22-APR-1994; 94US-0233606.

PR 22-FEB-1995; 95US-0393305.
 XX (IMV) IMMUNEX CORP.
 XX Grabstein KH, Wlmer MH;
 XX MPI: 1998-285678/25.
 XX N-PSDB: AAV23534.
 XX Use of Interleukin-15 - to enhance immunogenicity of a vaccine
 XX Disclosure: Column 5-6; 5pp; English.

XX This sequence is human Interleukin-15 (IL-15), which can be used in
 XX the vaccine of the invention. The vaccine composition comprises an
 XX immunogenic amount of a vaccine antigen (Ag) and an
 XX immunogenically augmenting amount of IL-15. The composition is useful for
 XX enhancing the immunogenicity of a vaccine. The cytokine IL-15 is a potent
 XX T and B cell growth factor. It causes proliferation and differentiation
 XX of these cells and augments T cell mediated immune responses. The vaccine
 XX composition can sufficiently elicit an immune response without being
 XX deleterious to the recipient, especially when using pathogenically
 XX deficient antigens. Some vaccines do not elicit a strong immune response
 XX and cannot provide sufficient protection on further exposure to the
 XX antigen.

Sequence 162 AA:

Query Match 100.0%; Score 833; DB 19; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-85;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRISKPHRSTISIOCYCLLNNSHFLTEAGIHVFLIGCFSAQIPTEANWNVISDLKI 60
 DB 1 MRISKPHRSTISIOCYCLLNNSHFLTEAGIHVFLIGCFSAQIPTEANWNVISDLKI 60
 OY 61 EDIISMHIDATLTYESDVHPSCVTAMKCFLELOVISLESGDASHDTVENLITLANN 120
 DB 61 EDIISMHIDATLTYESDVHPSCVTAMKCFLELOVISLESGDASHDTVENLITLANN 120
 OY 121 SLSNGNVTESGCKECEELEEKNIKEFLQSFVHIVOMFNTS 162
 DB 121 SLSNGNVTESGCKECEELEEKNIKEFLQSFVHIVOMFNTS 162

RESULT 9

AAM39185
 ID AAM39185 standard; Protein: 162 AA.

XX AAM39185;

XX 08-MAY-1998 (first entry)

XX Simian epithelium derived T-cell factor protein.

XX Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;
 XX B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
 XX treatment; prevention.

XX Simian.

XX Key

XX Peptide 1..48

XX Protein /label= leader sequence

XX US5707616-A.

XX 13-JAN-1998.

XX 04-OCT-1996; 96US-0726817.

PR 22-FEB-1995: 95US-0393305.
PR 08-MAR-1993: 93US-0031399.
PR 22-APR-1994: 94US-0233606.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;

XX WPI: 1998-100295/09.
DR N-PSDB; AAY02873.

XX Treatment or prevention of gastrointestinal diseases - by
PT administering epithelium-derived T-cell factor polypeptide

XX Disclosure; Column 35-38; 34pp; English.
XX This sequence represents a full length simian epithelium-derived T-cell
XX factor (ETP) which is used in a method for treating or preventing
XX gastrointestinal disease. These polypeptides have particular application
XX in the treatment of gastrointestinal disorders associated with disruption
XX of the gastrointestinal epithelium or villi such as chemotherapy- and
XX radiation-induced enteritis (gut toxicity), mucositis, peptic
XX ulcer disease, gastroenteritis and colitis. Villus atrophic disorders,
XX malignancy and inflammatory bowel disease. ETP polypeptides may also be
XX useful in the treatment of human immunodeficiency virus (HIV) and
XX HIV-associated disease due to their ability to stimulate CD4+ and CD8+
XX cells. Biologically active ETP may be used to treat a variety of other
XX diseases or conditions where T-cell or B cell stimulation is desired.

XX Sequence 162 AA:

Query Match 100.0%; Score 833; DB 19; Length 162;
Best Local Similarity 100.0%; Pred. NO. 2e-85;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRISKPHLRISIQCYLCILNSHFLTEAGIHVFIIGCFSGALPKPTFANWVVISDLKRI 60

DB 1 MRISKPHLRISIQCYLCILNSHFLTEAGIHVFIIGCFSGALPKPTFANWVVISDLKRI 60

QY 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISLESQASIHDPVENLIILANN 120

DB 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISLESQASIHDPVENLIILANN 120

QY 121 SLSNGNVTESGCKECELLEKNIKEFLQSFVHIVQMFINTS 162

DB 121 SLSNGNVTESGCKECELLEKNIKEFLQSFVHIVQMFINTS 162

RESULT 10
AAY03756
ID AAY03756 standard; Protein: 162 AA.

XX AAY03756;
XX 10-JUN-1999 (first entry)

XX Simian epithelium-derived T-cell factor (ETP) precursor polypeptide.
XX

XX Epithelium-derived T-cell factor; ETP; immunoassay; enteritis; ulcer;
XX T cell proliferation; gastrointestinal disease; mucositis; colitis;
XX gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;
XX human immune deficiency virus; tumour; simian.

XX Mammalia.
XX

XX US5892001-A.
XX

XX 06-APR-1999.
XX

XX 04-OCT-1996: 96US-0725969.
XX

XX 22-FEB-1995: 95US-0393305.
XX

PR 08-MAR-1993: 93US-0031399.
PR 22-APR-1994: 94US-0233606.
PR 04-OCT-1996: 96US-0725969.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;

XX WPI: 1999-253930/21.
DR N-PSDB; AAX29479.

XX Antibodies specific for epithelium-derived T-cell growth factor
PT Example 1; Columns 35-36; 34pp; English.

XX The invention relates to an isolated antibody that binds specifically to
XX a simian or human epithelium-derived T-cell factor (ETP) polypeptide. The
XX antibodies are used, optionally when immobilized or labeled, to detect
XX and quantify ETP in standard immunoassays. They may also be used as
XX diagnostic and therapeutic agents, e.g. when conjugated to toxins (or
XX their precursors) or radionuclides. ETP induces proliferation and/or
XX differentiation of T cells (or their precursors) e.g. for use in
XX establishing long term in vitro cultures; and is also used to treat
XX gastrointestinal disease (e.g. enteritis or mucositis induced by
XX chemotherapy or radiation, peptic ulcer, gastroenteritis, colitis,
XX villus atrophy, malignancy and inflammatory bowel disease), to treat
XX human immune deficiency virus infection or associated disease, or
XX generally in any situation requiring stimulation of T or B cell
XX proliferation, secretion of immunoglobulins or certain cytokines.
XX increased anti-infectious disease immunity, induction of T-cell lytic
XX activity or increased destruction of tumour or virus-infected cells. The
XX present sequence represents a simian ETP precursor polypeptide sequence.

XX Sequence 162 AA:

Query Match 100.0%; Score 833; DB 20; Length 162;
Best Local Similarity 100.0%; Pred. NO. 2e-85;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRISKPHLRISIQCYLCILNSHFLTEAGIHVFIIGCFSGALPKPTFANWVVISDLKRI 60

DB 1 MRISKPHLRISIQCYLCILNSHFLTEAGIHVFIIGCFSGALPKPTFANWVVISDLKRI 60

QY 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISLESQASIHDPVENLIILANN 120

DB 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELOVISLESQASIHDPVENLIILANN 120

QY 121 SLSNGNVTESGCKECELLEKNIKEFLQSFVHIVQMFINTS 162

DB 121 SLSNGNVTESGCKECELLEKNIKEFLQSFVHIVQMFINTS 162

RESULT 11
AAB18632
ID AAB18632 standard; Protein: 162 AA.

XX AAB18632;
XX 22-JAN-2001 (first entry)

XX Amino acid sequence of a human interleukin-4 helix A fragment.
XX

XX zaiaphali ligand; cytokine; haematopoietic cell proliferation; lymphoma;
XX tumorigenesis; leukaemia; hematopoiesis; B cell tumour; interleukin-4.

XX Homo sapiens.
XX

XX WO200053761-A2.
XX

XX 14-SEP-2000.
XX

XX 09-MAR-2000: 2000WO-US06067.
XX

XX 09-MAR-1999: 99US-0264908.
PR 11-MAR-1999: 99US-0265992.
PR 01-JUL-1999: 99US-0142013.
XX
XX (ZYMO) ZYMOGENETICS INC.

PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnson JV, Nelson AJ, Dillon SR, Hammond AK;
XX WPI: 2000-565600/52.
DR

PT New human cytokine, designated zalphall ligand, useful for stimulating
PT the proliferation and/or development of haematopoietic cells in vitro
PT and in vivo, and for treating tumourigenesis -
XX
PS Claim 10: Page 253-254; 256pp: English.

CC The present sequence represents part of a human interleukin-4. It
CC is used to produce fusion proteins with a human zalphall ligand.
CC zalphall ligand is a cytokine. The zalphall ligand is useful for
CC stimulating the proliferation and development of haematopoietic cells
CC in vitro and in vivo. Zalphall ligand polynucleotides can be used as
CC primers or probes for cloning the zalphall gene. The zalphall ligand is
CC useful for treating tumourigenesis. A zalphall ligand-saporin fusion
CC toxin may be used for treating leukaemias and lymphomas. Antagonists
CC against zalphall ligand are useful as research reagents for
CC characterizing expansion, proliferation, activation and differentiation
CC of cells involved in regulating haematopoiesis. The zalphall ligand may
CC also be used to stimulate an immune response against B cell tumour, a
CC virus, a parasite or a bacterium. The zalphall polypeptides,
CC polynucleotides, antagonists, agonists and antibodies are also useful
CC for the detection, diagnosis, prevention, and treatment of diseases
CC associated with a zalphall ligand genetic defect.

SO Sequence 162 AA:

Query Match 100.0%; Score 833; DB 21; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 162: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRISPHLRSTISIOCYCLILNSHFLTAGIHVFLIGCFSAQIPTEANWNVISDLKXI 60
DB 1 MRISPHLRSTISIOCYCLILNSHFLTAGIHVFLIGCFSAQIPTEANWNVISDLKXI 60
QY 61 EDLIQSMHIDATLVYTESDVHPSCKYTAMKCFLELOVISLESQDASHDVENLITLANN 120
DB 61 EDLIQSMHIDATLVYTESDVHPSCKYTAMKCFLELOVISLESQDASHDVENLITLANN 120
QY 121 SLSNGNVTESGCKECEELEEKNIKEFLQSFVHIYOMFINTS 162
DB 121 SLSNGNVTESGCKECEELEEKNIKEFLQSFVHIYOMFINTS 162

RESULT 12

AA78595
ID AAY78595 standard; Protein: 162 AA.

XX AAY78595;

XX 09-MAY-2000 (first entry)

DE Human interleukin-15 (IL-15) protein sequence.

KW Interleukin-15; IL-15; antagonist; irritable bowel disease; IBD;
KW celiac disease; treatment; human.

OS Homo sapiens.

XX MO200002582-A2.

XX 20-JAN-2000.

XX 09-JUL-1999: 99WO-GB02201.
XX
XX 10-JUL-1998: 98GB-0014892.
XX
XX (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.

PI Londei M, Quarantino S, Maiuri L;
XX WPI: 2000-171080/15.
DR N-PSDB: AAZ90032.

PT Use of antagonists of interleukin-15 for treating an inflammatory bowel
PT disease, particularly celiac disease -
XX
PS Disclosure: Page 69; 70pp: English.

CC This sequence represents the human interleukin 15 (IL-15) amino acid
CC sequence. The IL-15 nucleotide sequence and the protein encoded by it can
CC be used to determine and create antagonists of IL-15. An antagonist of
CC IL-15 can be used for treating an inflammatory bowel disease (IBD). The
CC invention relates to the treatment of celiac disease using IL-15
CC antagonists. The antagonists are preferably mutants of IL-15, antibodies
CC against IL-15 or IL-15 molecules bound to chemical groups that interfere
CC with the ability of IL-15 to effect a signal transduction through either
CC the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15
CC antagonists of the invention can be used to treat irritable bow disease
CC especially celiac disease.

SO Sequence 162 AA:

Query Match 100.0%; Score 833; DB 21; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 162: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRISPHLRSTISIOCYCLILNSHFLTAGIHVFLIGCFSAQIPTEANWNVISDLKXI 60
DB 1 MRISPHLRSTISIOCYCLILNSHFLTAGIHVFLIGCFSAQIPTEANWNVISDLKXI 60
QY 61 EDLIQSMHIDATLVYTESDVHPSCKYTAMKCFLELOVISLESQDASHDVENLITLANN 120
DB 61 EDLIQSMHIDATLVYTESDVHPSCKYTAMKCFLELOVISLESQDASHDVENLITLANN 120
QY 121 SLSNGNVTESGCKECEELEEKNIKEFLQSFVHIYOMFINTS 162
DB 121 SLSNGNVTESGCKECEELEEKNIKEFLQSFVHIYOMFINTS 162

RESULT 13

AA752308
ID AAY52308 standard; Protein: 162 AA.

XX AAY52308;

XX 09-FEB-2000 (first entry)

DE Simian epithelium-derived T-cell factor (ETF) precursor protein.

KW ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;
KW proliferation; differentiation; growth factor; precursor; mature; CD4+;
KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
KW gastrointestinal disease; gastroenteritis; colitis;
KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
KW tolerated dose.

OS Mammalia.

XX Key Location/Qualifiers

XX Peptide 1..48

XX Protein /note= "leader peptide"

XX /note= "mature simian ETF"

XX
Human interleukin 15 (IL-15) protein

121 SLSSNCAVTESGCKECEELEERNIKEFLQSHVHVIVQMEINTS 162

RESULT 15
AAB62012 standard; Protein; 162 AA.

AC AAB62012:

DT 14-MAY-2001 (first entry)

DE Simian ETF (SETF) polypeptide.

KW Epithelium-derived T-cell factor; ETF; simian; human; enteritis;
KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;
KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;
KW anti-HIV; antiviral; T-lymphocyte stimulator.

OS Mammalia.

FT Key Location/Qualifiers

FT Peptide 1..48

FT Protein /note= "leader sequence"

FT /note= "specifically claimed mature protein (AAB62013)"

PN US6184359-B1.

PD 06-FEB-2001.

PF 09-NOV-1998: 98US-0189193.

PR 22-FEB-1995: 95US-0393305.

PR 04-OCT-1996: 96US-0725969.

PR 08-MAR-1993: 93US-0031395.

PR 22-APR-1994: 94US-0233606.

PA (IMMUNEX) IMMUNEX CORP.

PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;

DR WPI: 2001-217801/22.

DR N-P-SDB: AAF57017.

PT New antibodies that specifically binds epithelium-derived T-cell factor
PT polypeptide useful for e.g. treating or preventing gastrointestinal
PT diseases, HIV and HIV-associated diseases, augmenting destruction of
PT tumour cells.

Example 1: Column 35-36; 35pp; English.

The invention relates to simian and human epithelium-derived T-cell
factor (ETF) polypeptides. Antibodies that specifically bind to the ETF
polypeptides are used for treating or preventing gastrointestinal
diseases, such as chemotherapy and radiation therapy-induced enteritis
and mucositis, peptic ulcer disease, villus atrophic disorders and
inflammatory bowel disease; for increasing tolerated doses for radiation
therapy and chemotherapy agents which are limited by gastrointestinal
toxicity; and for treating HIV and HIV-associated diseases. The
antibodies are further used to treat a variety of other diseases or
conditions where it is desired to stimulate proliferation of
T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
LAK or NK lytic activity, or to augment the destruction of tumour cells
or cells infected with virus. The present sequence represents the
simian ETF (SETF) polypeptide.

Sequence 162 AA:

Query Match

Best Local Similarity 100.0%; Score 833; DB 22; Length 162;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRLSKPHLRISISIQCYCLLLNSHFLTEAGIHVFLTGCFSAGLPKTEANWVNSDLKI 60
|||||

DB 1 MRLSKPHLRISISIQCYCLLLNSHFLTEAGIHVFLTGCFSAGLPKTEANWVNSDLKI 60
QY 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLEFLOYISLESGDASTIDYVENIILANN 120
DB 61 EDLIQSMHIDATLYTESDVHPSCKVTAMKCFLEFLOYISLESGDASTIDYVENIILANN 120
QY 121 SLSSNGNVTESGCKECELEEKNIKEFLQSFVHIQVMTNTS 162
DB 121 SLSSNGNVTESGCKECELEEKNIKEFLQSFVHIQVMTNTS 162

Search completed: February 20, 2003, 16:28:24
Job time : 34 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2003, 16:27:12 : Search time 23.5 Seconds
(without alignments)
662.714 Million cell updates/sec

Title: us-09-855-313a-4
Perfect score: 833
Sequence: 1 MRISKPHLRISISIQCYLCLL.....NIKEFLQSFVHIYOMFINTS 162

Scoring table:
BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:.*
2: PIR1:.*
3: PIR2:.*
4: PIR3:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	805	96.6	162	1 A53484	Interleukin-15 pre
2	626	75.2	162	2 I49124	Interleukin-15 - m
3	96.5	11.6	433	2 H97846	hypothetical prote
4	95	11.4	517	2 S36712	FUN26 protein - ye
5	88.5	10.6	500	2 T28168	hypothetical prote
6	85	10.2	510	2 T11943	NADH2 dehydrogenas
7	84	10.2	1799	2 AD1895	serine/threonine k
8	83.5	10.1	928	2 T04192	hypothetical prote
9	83.5	10.0	595	1 A48077	myb-related protei
10	82.5	9.9	477	2 T46666	N-ethylameline ch
11	81.5	9.8	3394	2 T18501	hypothetical prote
12	80.5	9.7	642	2 T28866	hypothetical prote
13	80.5	9.7	922	2 T03854	hypothetical prote
14	80.5	9.7	1070	2 G84982	exodeoxyribonuclea
15	79.5	9.5	364	2 C64047	proliferin (proline
16	79	9.5	197	2 G72286	hypothetical prote
17	79	9.5	456	2 S20597	hypothetical prote
18	78	9.4	319	2 B81382	ribonuclease 1n1b
19	78	9.4	646	2 A11174	ltyclophan-tRNA 1i
20	77.5	9.3	229	2 T34325	interthalin, probab
21	77.5	9.3	902	2 A56823	hypothetical prote
22	77.5	9.3	911	2 S51441	DNA-directed RNA p
23	77.5	9.3	1353	2 S11691	hypothetical prote
24	77	9.2	250	2 A11366	regulatory protein
25	77	9.2	527	2 S53835	NADH2 dehydrogenas
26	76.5	9.2	707	2 S57157	hypothetical prote
27	76.5	9.2	707	2 T28177	hypothetical prote
28	76.5	9.2	810	2 T44430	protein PV100 (imp
29	76	9.1	767	1 COZPCD	cdc10 start contro

30	76	9.1	938	2 T41932	hypothetical prote
31	75.5	9.1	670	2 E86164	PI5K3.10 protein -
32	75.5	9.1	729	2 A49120	Fibroblast growth
33	75.5	9.1	1113	2 T26954	hypothetical prote
34	75.5	9.1	1336	2 S41794	SEC3 protein - yea
35	75	9.0	130	2 C66820	hypothetical prote
36	75	9.0	307	2 B38448	acylttransferase (E
37	75	9.0	468	2 T05602	cytochrome P450 -
38	75	9.0	820	2 T05602	hypothetical prote
39	75	9.0	849	2 C97303	hypothetical prote
40	75	9.0	1021	2 T42634	connectin/titin -
41	74.5	8.9	387	2 E64688	hypothetical prote
42	74.5	8.9	598	2 F75212	glutamine-fructose
43	74.5	8.9	617	2 D96978	hypothetical prote
44	74.5	8.9	809	2 S64594	probable beta-adap
45	74.5	8.9	1630	2 S64403	Espr1 protein - yea

ALIGNMENTS

RESULT 1

A53484
Interleukin-15 precursor - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A53484

R:Gradshteyn, K.R.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.; Gitt, J.G.

Science 264, 965-968, 1994

A:Title: Cloning of a T cell growth factor that interacts with the beta chain of the

A:Reference number: A53484; MUID:94233380; PMID:8178155

A:Accession: A53484

A:Status: nucleic acid sequence not shown

A:Cross-References: GB:U03099; NID:9493521; PIDN:AAAI8416.1; PID:9493522

A>Note: The complete translation is not shown

C:Superfamily: Interleukin-15

C:Keywords: growth factor

F:49-162/Product: Interleukin-15 #status predicted <MAT>

F:83-133,90-136/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 96.6%; Score 805; DB 1; Length 162;

Matches 136; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRISKPHLRISISIQCYLCLLNSHFLTEAGIHVFLIGCSAGLPRTKMWVYISDLKRI 60

Db 1 MRISKPHLRISISIQCYLCLLNSHFLTEAGIHVFLIGCSAGLPRTKMWVYISDLKRI 60

QY 61 EDLQSMHIDTLTYTSDVHPSCKYTANKCFLELOVISLSDGASLHDIVENLILVANN 120

Db 61 EDLQSMHIDTLTYTSDVHPSCKYTANKCFLELOVISLSDGASLHDIVENLILVANN 120

QY 121 SLSSNGVNTSECKECELLEKNKEFLQSFVHIYOMFINTS 162

Db 121 SLSSNGVNTSECKECELLEKNKEFLQSFVHIYOMFINTS 162

QY 121 ILSSNGNTSECKECELLEKNKEFLQSFVHIYOMFINTS 162

Db 121 ILSSNGNTSECKECELLEKNKEFLQSFVHIYOMFINTS 162

RESULT 2

I49124
Interleukin-15 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 16-Jul-1999

C:Accession: I49124

R:Anderson, D.M.; Johnson, L.; Glaccum, M.B.; Copeland, N.G.; Gilbert, D.J.; Jenkins,

Genomics 25, 701-706, 1995

A:Title: Chromosomal assignment and genomic structure of IL15.

A:Reference number: A56005; MUID:95278940; PMID:7759105

A:Accession: I49124

A:Status: preliminary

A:Molecule type: mRNA

A:Reference number: S36711

0x 129 TEGCKECELEKNIK-----EFLÖSFVHIÖMFINTS 162

Db 267 S-----DCKKLPVSLKMGVCYCYIVDFKFLPELITNLOKLNISN 306

RESULT 6

T11943

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Prototheca wickerhamii mitochondrion

C:Species: mitochondrion Prototheca wickerhamii

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002

C:Accession: T11943

R:Wolff, G.; Plante, I.; Lang, B.F.; Koeck, U.; Burger, G.

J. Mol. Biol. 237, 75-86, 1994

A:Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Prototheca

A:Reference number: 217373; M01D:94180393; PMID:8133522

A:Accession: T11943

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-510 <MOL>

A:Cross-references: EMBL:002970; NID:9467843; PID:9467875; PIDN:AAD12662.1

A:Experimental source: strain 263-11

C:Genetics:

A:Genome: mitochondrion

A:Note: nad2

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 10.2%; Score 85; DB 2; Length 510;

Best Local Similarity 50.0%; Pred. No. 5.2;

Matches 18; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Db 157 LQSLISQICVLCCLLNHSHFTEGHHVFILCCFSAGL 43

157 LQSLISQICVLCCLLNHSHFTEGHHVFILCCFSAGL 192

RESULT 7

AD1895

serine/threonine kinase with two-component sensor domain alr0710 [imported] - Nostoc sp.

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AD1895

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi, S.

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; M01D:21595285; PMID:11759840

A:Accession: AD1895

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1799 <KOR>

A:Cross-references: GB:BA000019; PIDN:BA072667.1; PID:917130055; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr0710

Query Match 10.2%; Score 85; DB 2; Length 1799;

Best Local Similarity 22.4%; Pred. No. 23;

Matches 39; Conservative 28; Mismatches 57; Indels 50; Gaps 7;

Db 36 LCGFSAGLPKTEAMVWVYSDK-----KIDLIQSMHIDATLYTESVYPSCK 84

1552 LCGFSAGLPKTEAMVWVYSDK-----KIDLIQSMHIDATLYTESVYPSCK 1608

85 VYAMKCFLE-----LOVSLSSGD-----ASHDYENLITLANSLSN-----125

1609 AMIMACNLENIISTLRTSRADKDYKVKFVHGGIDSTILLKRLKANOQHPALEVT 1668

126 --GNTESGC-----KECELEKNI--KEFLQSFVIVOMPLNS 162

1669 NTGDLPLVNCPPQGLNOVPMVITLAINADALEANICKSPAFITAPRITITS 1722

RESULT 8

T04192

hypothetical protein T4P9.30 - Arabidopsis thaliana

N:Alternate names: protein T4P9.30

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

C:Accession: T04192

R:Bevan, M.; Medler, H.; Medler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Meyer, K.

submitted to the Protein Sequence Database, March 1999

A:Reference number: 215260

A:Accession: T04192

A:Molecule type: DNA

A:Residues: 1-928 <BEV>

A:Cross-references: EMBL:AL049523

A:Experimental source: cultivar Columbia; BAC clone T4P9

C:Genetics:

A:Map position: 4

A:Insertions: 51/2; 122/2; 161/3; 181/3; 214/3; 328/1; 401/3; 458/3; 544/3; 596/2; 774/2

A:Note: T4P9.30

Query Match 10.1%; Score 84; DB 2; Length 928;

Best Local Similarity 25.9%; Pred. No. 13;

Matches 36; Conservative 25; Mismatches 54; Indels 24; Gaps 7;

Db 7 HURSTICVLCCLLNHSHFTEGHHVFILCCFSAGLPKTEAN-W-----VNTS 55

137 YTRSYVEVPLCLMLTDGRDSRTASIRELYECAMGVPOEKAHIMWDFDKRNGLL 196

56 D---LKKIEDLIQSMHIDATLYTESDVHPSCKVYAMKCFLELOVITSGDASHIDIVE 112

197 DPLSKSLER--SLHMODDILVEVDGLSSSSQSMSTGNEALVLEPS-----R 246

Db 113 NLIILANSSLSNGNTES 131

247 STVITACGPTLSNGSTTS 265

RESULT 9

A48077

myb-related protein REB1 - yeast (Kluyveromyces marxianus var. lactis)

C:Species: Kluyveromyces marxianus var. lactis; Candida sphaerica

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999

C:Accession: A48077

R:Morrow, B.E.; Yu, O.; Warner, J.R.

Mol. Cell. Biol. 13, 1173-1182, 1993

A:Title: A bipartite DNA-binding domain in yeast Reb1p.

A:Reference number: A48077; M01D:93140755; PMID:8423784

A:Accession: A48077

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-595 <MOR>

A:Cross-references: GB:J03789; NID:q173313; PIDN:AA61343.1; PID:q173314

A:Note: sequence extracted from NCBI backbone (NCBIN:123574, NCBI:P:123576)

C:Superfamily: myb-related protein REB1; myb DNA-binding repeat homology

C:Keywords: DNA binding; nucleus; transcription regulation

P:333-382/Domain: myb DNA-binding repeat homology <MYB>

Query Match 10.0%; Score 83.5; DB 1; Length 595;

Best Local Similarity 25.0%; Pred. No. 8.6;

Matches 28; Conservative 24; Mismatches 51; Indels 9; Gaps 2;

Db 44 PTEAMVWVYSDKRTIEDLIQSMHIDATLYTESDVHPSCKVYAMKCFLELOVITSLSG 103

183 PKKESERSSTGDSNIDHVDVSVSGSIPSOVRLKTAELV-----KVLSSSH 234

104 DASHDYENLITLANSLSNGN-VYTESGCKCELEKNIKEFLQSFVHI 154

235 NDDODDVSNILOEAAKASHIINPATONGSKSFDESEELALPFIKEYOKI 286

RESULT 10

T46666

N-ethylmaleline chlorohydroxylase [validated] - Rhodococcus corallinus

RESULT 12
T28866
hypothetical protein R03M4.1 - *Caenorhabditis elegans*
C; Species: *Caenorhabditis elegans*

RESULT 14

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2003, 16:27:07 ; Search time 16.5 Seconds
(without alignments) 407.222 Million cell updates/sec

Title: US-09-855-313a-4
Perfect score: 833
Sequence: 1 MRSKPHRSISIOCYLCLL.....NIKEFLQSFVHIVQMFINTS 162

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83.5	100.0	162	1	IL15_HUMAN
2	81.0	97.2	162	1	IL15_MACHO
3	80.5	96.6	162	1	IL15_CERAE
4	69.0	82.8	162	1	IL15_FELCA
5	66.2	79.5	162	1	IL15_PIG
6	65.2	78.3	162	1	IL15_BOVIN
7	65.0	78.0	162	1	IL15_SHEEP
8	62.6	75.2	162	1	IL15_MOUSE
9	61.7	74.1	162	1	IL15_RAT
10	95	11.4	517	1	PU26_YEAST
11	83.5	10.0	595	1	REB1_KIOLA
12	82.5	9.9	476	1	TRPA_RHOC
13	81	9.7	269	1	TRPA_BUCSC
14	80.5	9.7	1070	1	EXSC_BUCAL
15	79	9.5	456	1	RINI_RAT
16	79	9.5	560	1	HCYG_SEPOF
17	77.5	9.3	902	1	REB1_DICDI
18	77	9.2	527	1	NU2M_ACACA
19	77	9.2	707	1	YJ9C_YEAST
20	76	9.1	491	1	HSPI_CHICK
21	76	9.1	767	1	CC10_SCHPO
22	76	9.1	938	1	V120_HSV7
23	75.5	9.1	730	1	FGRI_DROME
24	75.5	9.1	1336	1	SECI_YEAST
25	75	9.0	307	1	LX02_PHOUL
26	75	9.0	490	1	CPCL_HUMAN
27	74.5	8.9	597	1	GIMS_PYRAB
28	74.5	8.9	809	1	ADBB_YEAST
29	74.5	8.9	1630	1	ESPI_YEAST
30	73.5	8.8	355	1	HIST_BUCAP
31	73.5	8.8	948	1	CDAA_HUMAN
32	73	8.8	497	1	NU2M_CHOCR
33	73	8.8	4393	1	PGBM_HUMAN

ALIGNMENTS

RESULT 1	IL15_HUMAN	STANDARD:	PRT:	162 AA.
ID	IL15_HUMAN			
DT	P40933; Q93058; Q43512; Q00440; Q9UBA3;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Interleukin-15 precursor (IL-15).			
GN	IL15.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (IL15-S48A ISOFORM).			
KC	TISSUE=Bone marrow;			
RX	MEDLINE=94233380; PubMed=8178155;			
RA	Grabstein K.K., Eisenman J., Sheenbeck K., Rauch C.,			
RA	Srinivasan S., Fung V., Beers G., Richardson J., Schoenborn M.A.,			
RA	Abdieh M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,			
RA	Giri J.G.;			
RT	"Cloning of a T cell growth factor that interacts with the beta chain			
RT	of the interleukin-2 receptor.";			
RL	Science 264:965-968(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A. (IL15-S48A ISOFORM).			
RA	Krause H., Jandrig B., Wernicke C., Bulfone-Paus S., Pohl T.,			
RA	Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A. (IL15-S21AA ISOFORM).			
KC	TISSUE=Lung cancer;			
RX	MEDLINE=96218668; PubMed=8668345;			
RA	Meazza R., Verdiani S., Blassoni R., Coppolecchia M., Gaggero A.,			
RA	Orengo A.M., Colombo M.P., Azzone B., Ferrini S.;			
RT	"Identification of a novel interleukin-15 (IL-15) transcript isoform			
RT	generated by alternative splicing in human small cell lung cancer			
RL	cell lines.";			
RN	Oncogene 12:2187-2192(1996).			
RP	SEQUENCE FROM N.A. (IL15-S21AA ISOFORM).			
KC	TISSUE=Testis;			
RX	MEDLINE=98070771; PubMed=9405632;			
RA	Tagaya Y., Kurys G., Thies T.A., Losi J.M., Azimi N., Hanover J.A.,			
RA	Bamford R.N., Waldmann T.A.;			
RT	"Generation of secretable and nonsecretable interleukin 15 isoforms			
RT	through alternate usage of signal peptides.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1444-1449(1997).			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RA	Meazza R., Ferrini S.;			
RT	"Expression of two IL-15 mRNA isoforms in human tumors does not			
RT	correlate with secretion: role of different signal peptides.";			
RL	Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 49-162 FROM N.A.			

P30550 homo sapien
Q94655 plasmodium
P48120 cyanophora
P10775 sus scrofa
O00629 homo sapien
Q9Y242 homo sapien
Q43847 homo sapien
P04050 saccharomyc
O01352 drosophila
O14824 homo sapien
P20471 rhizobium m
O24735 sulfolobus

```

IL15_Macaca
P48092:
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Interleukin-15 precursor (IL-15).
IL15.
Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Carniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
NCBI_TaxId:9544;
[1]
SEQUENCE FROM N.A.
TISSE-Blood;
MEDLINE:96003435; PubMed:7561102;
Vallinger F.J., Brar S.S., Mayne A.E., Chikata N., Ansari A.A.;
"Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
J. Immunol. 155:3946-3954(1995).
[2]
SEQUENCE FROM N.A.
Tatsumi M.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
GAMMA BUT NOT IL-2R ALPHA.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
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EMBL: U19843; AAB60398.1; -
EMBL: AB000555; BAA19149.1; -
InterPro: IPR003443; Interleukin_15.
Pfam: PF02372; IL15; 1.
Cytokine; Glycoprotein; signal.
SIGNAL 1 29 POTENTIAL.
PROPEP 30 48 POTENTIAL.
CHAIN 49 162 INTERLEUKIN_15.
DISULFID 83 133 POTENTIAL.
DISULFID 90 136 POTENTIAL.
CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
VARIANT 5 5 K > T.
VARIANT 31 31 I -> T.
SEQUENCE 162 AA; 18194 MW; D233CF7F6186C01 CRC64;

Query Match 97.2%; Score 810; DB 1; Length 162;
Best local similarity 96.3%; Pred. No. 2, 8e-67;
Matches 156; Conservative 2; Mismatches 4; Indels 0; Gaps 0.

QY 1 MRISKPLRSLSIQCYICLLLNSHFTTEAGIHVILIGCFSAQLPTEANVNVISDLKRI 60
Db 1 MRISKPLRSLSVSIQCYICLLLNHSHFTTEAGIHVILIGCFSAQLPTEANVNVISDLKRI 60

QY 61 EDLIQSMHIDATILYTESDVHPSCKVTAMKCELELOVYISIESGDMSIHDTVEMLILANN 120
Db 61 EDLIQSMHIDATILYTESDVHPSCKVTAMKCELELOVYISIESGDSDIHDTVEMLILANN 120

QY 121 SLISNGNVTSCGKCECELEFNKIKFELOSFYHIVQMFIINTS 162
Db 121 SLISNGNVTSCGKCECELEFNKIKFELOSFYHIVQMFIINTS 162

QY 121 SLISNGNVTSCGKCECELEFNKIKFELOSFYHIVQMFIINTS 162
Db 121 SLISNGNVTSCGKCECELEFNKIKFELOSFYHIVQMFIINTS 162

```

IL15_CERAE
 ID IL15_CERAE STANDARD: PRT: 162 AA.
 AC P40221;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-15 precursor (IL-15).
 GN IL15.
 OS Cercopithecus aethiops (Green monkey) (Griwet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecidae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SOURCE FROM N.A., AND SEQUENCE OF 49-81.
 RC TISSUE=Kidney;
 RX MEDLINE=9423380; PubMed=8178155;
 RA Graubstein K.H., Eisenman J., Shanebeck K., Rauch C.,
 RA Srinivasan S., Fung V., Beers C., Richardson J., Schoenborn M.A.,
 RA Abdieh M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,
 RA Gird J.G.;
 RT "Cloning of a T cell growth factor that interacts with the beta chain
 of the interleukin-2 receptor.";
 RL Science 264:965-968(1994).
 CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 GAMMA BUT NOT IL-2R ALPHA.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U03099; AAA18416.1;
 DR InterPro: IPR003443; Interleukin_15.
 DR Pfam: PF02372; IL15; 1
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 48
 FT CHAIN 49 162 INTERLEUKIN-15.
 FT DISULFID 83 133 POTENTIAL.
 FT DISULFID 90 136 POTENTIAL.
 FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 162 AA; 18222 MW; 18F9A8264DE1C9B7 CRC64;
 SO SEQUENCE

Query Match 96.6%; Score 805; DB 1; Length 162;
 Best local similarity 96.3%; Pred. No. 8e-67;
 Matches 156; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRISPKHLRSTISQCYCLLLNSHFLTEAGIHVFLIGCFSAQIPKTEANNVVISDLKTI 60
 DB 1 MRISPKHLRSTISQCYCLLLNSHFLTEAGIHVFLIGCFSAQIPKTEANNVVISDLKTI 60
 QY 61 EDLIQSMHIDATLTYSQVDSVHPSCKYTAMKCFLELOVISLESQASHTDVENLILANN 120
 DB 61 EDLIQSMHIDATLTYSQVDSVHPSCKYTAMKCFLELOVISLESQASHTDVENLILANN 120
 QY 121 SSSNGVNTSGCKECEELEENKIKFLOSFAHIVOMFINTS 162
 DB 121 SSSNGVNTSGCKECEELEENKIKFLOSFAHIVOMFINTS 162
 QY 121 ILSSNGNTSGCKECEELEENKIKFLOSFAHIVOMFINTS 162
 DB 121 ILSSNGNTSGCKECEELEENKIKFLOSFAHIVOMFINTS 162

RESULT 4
 IL15_FEICA
 ID IL15_FEICA STANDARD: PRT: 162 AA.
 AC 097687;
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-15 precursor (IL-15).
 GN IL15.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SOURCE FROM N.A.
 RC TISSUE=Lymph node;
 RA Barger A.B., Dean G.A., Layoy A.S.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBP databases.
 CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF108148; AAD05268.1;
 DR InterPro: IPR003443; Interleukin_15.
 DR Pfam: PF02372; IL15; 1
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 48
 FT CHAIN 49 162 INTERLEUKIN-15.
 FT DISULFID 83 133 POTENTIAL.
 FT DISULFID 90 136 POTENTIAL.
 FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 162 AA; 18412 MW; D8C7CEFF7F40110DD CRC64;
 SO SEQUENCE

Query Match 82.8%; Score 690; DB 1; Length 162;
 Best local similarity 82.7%; Pred. No. 2.6e-56;
 Matches 134; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MRISPKHLRSTISQCYCLLLNSHFLTEAGIHVFLIGCFSAQIPKTEANNVVISDLKTI 60
 DB 1 MRISPKHLRSTISQCYCLLLNSHFLTEAGIHVFLIGCFSAQIPKTEANNVVISDLKTI 60
 QY 61 EDLIQSMHIDATLTYSQVDSVHPSCKYTAMKCFLELOVISLESQASHTDVENLILANN 120
 DB 61 EDLIQSMHIDATLTYSQVDSVHPSCKYTAMKCFLELOVISLESQASHTDVENLILANN 120
 QY 121 SSSNGVNTSGCKECEELEENKIKFLOSFAHIVOMFINTS 162
 DB 121 SSSNGVNTSGCKECEELEENKIKFLOSFAHIVOMFINTS 162
 QY 121 GLSSNRNTTSGCKECEELEENKIKFLOSFAHIVOMFINTS 162
 DB 121 GLSSNRNTTSGCKECEELEENKIKFLOSFAHIVOMFINTS 162

RESULT 5
 IL15_PIG
 ID IL15_PIG STANDARD: PRT: 162 AA.
 AC 095253;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-15 precursor (IL-15).
 GN IL15.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SOURCE FROM N.A.

[illegible]

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DR EMBL: A149700; AAD37425.1; -
 DR InterPro: IPR003443; Interleukin_15.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 48
 FT CHAIN 49 162
 FT DISULFID 83 133
 FT DISULFID 90 136
 FT CARBOHYD 113 113
 FT CARBOHYD 121 121
 FT CARBOHYD 127 127
 SQ SEQUENCE 162 AA: 18510 MW: 8719565043F1E5D0 CRC64;
 N-LINKED (GLCNAC...) (POTENTIAL).
 N-LINKED (GLCNAC...) (POTENTIAL).
 N-LINKED (GLCNAC...) (POTENTIAL).

Query Match
 Best Local Similarity 77.8%; Score 650; DB 1; Length 162;
 Matches 126; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

OY 1 MRISKPLRSISIOCYLCILNHSFLEAGIHVFTLGCFSAGLPKTEANWVVISDLKRI 60
 DB 1 MKILKPYMRNTSISCYLCFLNHSFLEAGIHVFTLGCFSAGLPKTEANWVVISDLKRI 60
 OY 61 EDLQSHMDATLTYESDVHPSCKVTAMKCFLELOVTSLESGDASIHPTVENLITLANN 120
 DB 61 EHLQSHMDATLTYESDVHPSCKVTALQCFLELRLVTHESNNAIYEITLNTLMLADR 120
 OY 121 SLSSNGVNESGCKCELEEKNIKEFLQSFVHIQVOMFINTS 162
 DB 121 TLSNKNVAESGCKCELEEKNIKEFLQSFVHIQVOMFINTS 162

RESULT 8
 ID IL15_MOUSE STANDARD: PRT: 162 AA.
 AC P48346;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-15 precursor (IL-15).
 GN IL15.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WC/REL X C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=95278940; PubMed=7759105;
 RA Anderson D.M., Johnson L., Glaccum M.B., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Valentine V., Kirstein M.N., Shapiro D.N., Morris S.W.,
 RA Grabstein K., Cosman D.;
 Chromosomal assignment and genomic structure of IL15.
 RL Genomics 25:701-706(1995)
 RT
 RL FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 GAMMA BUT NOT IL-2R ALPHA.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 SIMILARITY: BELONGS TO THE IL-15 FAMILY.

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DR EMBL: U14332; AAA75377.1; -
 DR MGD: MGI:103014; IL15.
 DR InterPro: IPR003443; Interleukin_15.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 29
 FT PROPEP 30 48
 FT CHAIN 49 162
 FT DISULFID 83 133
 FT DISULFID 90 136
 FT CARBOHYD 104 104
 FT CARBOHYD 108 108
 FT CARBOHYD 119 119
 SQ SEQUENCE 162 AA: 18593 MW: 669371498CEBF296 CRC64;
 N-LINKED (GLCNAC...) (POTENTIAL).
 N-LINKED (GLCNAC...) (POTENTIAL).
 N-LINKED (GLCNAC...) (POTENTIAL).

Query Match
 Best Local Similarity 75.2%; Score 626; DB 1; Length 162;
 Matches 118; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

OY 1 MRISKPLRSISIOCYLCILNHSFLEAGIHVFTLGCFSAGLPKTEANWVVISDLKRI 60
 DB 1 MKILKPYMRNTSISCYLCFLNHSFLEAGIHVFTLGCFSAGLPKTEANWVVISDLKRI 60
 OY 61 EDLQSHMDATLTYESDVHPSCKVTAMKCFLELOVTSLESGDASIHPTVENLITLANN 120
 DB 61 EHLQSHMDATLTYESDVHPSCKVTAMKCFLELRLVTHESNNAIYEITLNTLMLADR 120
 OY 121 SLSSNGVNESGCKCELEEKNIKEFLQSFVHIQVOMFINTS 162
 DB 121 TLSNKNVAESGCKCELEEKNIKEFLQSFVHIQVOMFINTS 162

RESULT 9
 ID IL15_RAT STANDARD: PRT: 162 AA.
 AC P97604; 054847;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Interleukin-15 precursor (IL-15).
 GN IL15.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG FORM).
 RC STRAIN=Sprague-Dawley; TISSUE=Jejunum;
 RX MEDLINE=97098212; PubMed=8542753;
 RA Reinecker H.C., Macdermott R.P., Miran S., Dignass A., Podolsky D.K.,
 RA *Intestinal epithelial cells both express and respond to interleukin
 RT 15.*;
 RL Gastroenterology 111:1706-1713(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
 RC STRAIN=Wistar; TISSUE=Spleen;
 RA Park J.-H.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 SIMILARITY: BELONGS TO THE IL-15 FAMILY.

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CC EMBL: U69272: ABA1697.1: -
 CC EMBL: AF015719: AAB94536.1: -
 DR EMBL: AF015718: AAB94535.1: -
 DR InterPro: IPR003443: Interleukin_15.
 DR Pfam: PF02372: IL15: 1.
 DR Cytokine: Glycoprotein; Signal: Alternative splicing.
 KM SIGNAL: 1
 FT PROPEP 30 48 POTENTIAL.
 FT CHAIN 49 162 INTERLEUKIN-15.
 FT DISULFID 83 133 POTENTIAL.
 FT DISULFID 90 136 POTENTIAL.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 81 96 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 162 AA: 18804 MW: 166097AB3055ADA CRC64:
 Query Match 74.1%; Score 617; DB 1; Length 162;
 Best Local Similarity 72.2%; Pred. No. 1.2e-49;
 Matches 117; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

QY 1 MKISPKHRSISIOCYCLLLNSHFLHAGIHVFLICGFSAGLPTKAMVNVISDLKRI 60
 1 MKILKPYWRNTSLIYLCFLNSHFLHAGIHVFLICGFSAGLPTKAMVNVISDLKRI 60
 DB 1 MKILKPYWRNTSLIYLCFLNSHFLHAGIHVFLICGFSAGLPTKAMVNVISDLKRI 60

QY 61 EDLIOSMHIDATVETSDVHPSCVYAMKCFLELOVISLESQASIHQVEMLIILANN 120
 61 ESDIHFHIDTTLTSDPHPSCKVTANCFLELOVILHEXSNMTNETVRVLYLANS 120
 DB 61 ESDIHFHIDTTLTSDPHPSCKVTANCFLELOVILHEXSNMTNETVRVLYLANS 120

QY 121 SLSSNGNVTESGCEKECELEENIKFLOSFVHIVOMFINTS 162
 121 TLLSNKNVIESGCKECELEENIKFLOSFVHIVOMFINTS 162
 DB 121 TLLSNKNVIESGCKECELEENIKFLOSFVHIVOMFINTS 162

RESULT 10
 FU26_YEAST STANDARD; PRI: 517 AA.
 ID FU26_YEAST STANDARD; PRI: 517 AA.
 AC P31381;
 DT 01-JUL-1993 (rel. 26, Last sequence update)
 DT 01-JUL-1993 (rel. 26, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Nucleoside transporter FUN26.
 GN FUN26 OR VAL022C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5286c / A8972;
 RX MEDLINE=93209532; PubMed=8458570;
 RA Ouellette B.F., Clark M.W., Keng T., Storms R.K., Zhong W.W.,
 Zeng B., Fortin N., Delaney S., Barton A.B., Kaback D.B., Bussey H.;
 "Sequencing of chromosome I from Saccharomyces cerevisiae: analysis
 of a 32 kb region between the IRI1 and SPO7 genes."
 RT Genome 36:32-42(1993).
 RL [2]
 RP CHARACTERIZATION.
 RX MEDLINE=20408929; PubMed=10827169;
 RA Vickers M.F., Yao S.Y., Baldwin S.A., Young J.D., Cass C.E.;
 "Nucleoside transporter proteins of Saccharomyces cerevisiae.
 demonstration of a transporter (FU11) with high uridine selectivity
 in plasma membranes and a transporter (FUN26) with broad nucleoside
 selectivity in intracellular membranes."
 RT J. Biol. Chem. 275:25931-25938(2000).
 RL J. Biol. Chem. 275:25931-25938(2000).
 CC -1- FUNCTION: HAS BROAD NUCLEOSIDE SELECTIVITY (URIDINE, ADENOSINE AND
 CYTIDINE) AND MOST LIKELY FUNCTIONS TO TRANSPORT NUCLEOSIDES
 ACROSS INTRACELLULAR MEMBRANES.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-1- SIMILARITY: BELONGS TO THE SUC29A FAMILY OF TRANSPORTERS.

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CC EMBL: I05146: AAC04935.1: -
 DR PIR: S36712: S36712.
 DR SGD: S0000020: FUN26.
 DR InterPro: IPR002259: DER/eqnu_transpt.
 DR Pfam: PF01733: Nucleoside_tran: 1.
 DR Prodom: PD005103: DER/eqnu_transpt: 1.
 DR TIGRfam: TIGR00939: 2a57.1.
 KW Transmembrane; Transport.
 FT TRANSMEM 76 96 POTENTIAL.
 FT TRANSMEM 116 136 POTENTIAL.
 FT TRANSMEM 151 171 POTENTIAL.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 214 234 POTENTIAL.
 FT TRANSMEM 243 263 POTENTIAL.
 FT TRANSMEM 344 364 POTENTIAL.
 FT TRANSMEM 367 387 POTENTIAL.
 FT TRANSMEM 411 431 POTENTIAL.
 FT TRANSMEM 446 466 POTENTIAL.
 FT TRANSMEM 492 512 POTENTIAL.
 SQ SEQUENCE 517 AA: 58317 MW: 43922A3E9A3D8D50 CRC64:
 Query Match 11.4%; Score 95; DB 1; Length 517;
 Best Local Similarity 25.2%; Pred. No. 0.26; 71; Indels 18; Gaps 5;
 Matches 40; Conservative 30; Mismatches 71; Indels 18; Gaps 5;

QY 16 YLCILLNSHFLTEAGIHVFLICGFSAGLPTKAMVNVISDLKRIEDLIOSMHIDATLXT 75
 343 YLVLSITFTVTLVTPVAFASATVYTGPLSNQYIPDLFTLMLGSLYRTADMPWR 402

QY 76 ESDVHPS-----CKVTAMKCFLELOVISLESQASIHQVEMLIILANNLS----- 123
 403 DQKFTPKRTFTYSLRVAAPLELMTVAITSSSGDEHNSV--YVLCYMLQGLFGV 460

DB 403 DQKFTPKRTFTYSLRVAAPLELMTVAITSSSGDEHNSV--YVLCYMLQGLFGV 460

QY 124 SNGNV-TEGCKECELEENIKFLOSFVHIVOMFINT 161
 461 TNGHVSMSFMKVEQDLNDEKAAAGFTNI--FVST 496

RESULT 11
 REB1_KLJUA STANDARD; PRI: 595 AA.
 ID REB1_KLJUA STANDARD; PRI: 595 AA.
 AC Q05950;
 DT 01-FEB-1995 (rel. 31, Created)
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE DNA-binding protein REB1 (QBP).
 GN REB1.
 OS Kluyveromyces fragilis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93140755; PubMed=8423784;
 RA Morrow B.E., in O., Warner J.R.;
 "A bipartite DNA-binding domain in yeast Reb1p."
 Mol. Cell. Biol. 13:1173-1182(1993).
 CC -1- FUNCTION: DNA-BINDING PROTEIN THAT RECOGNIZES SITES WITHIN BOTH
 CC THE ENHANCER AND THE PROMOTER OF RNA TRANSCRIPTION, AS WELL AS
 CC UPSTREAM OF MANY GENES TRANSCRIBED BY RNA POLYMERASE II. IT IS
 CC SPECIFICALLY RECOGNIZE THE SEQUENCE 5'-CGGAGTA-3' OR 5'-CGGCTTR-3'
 CC (WHERE R IS ANY PURINE) (BY SIMILARITY).

```

CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: L03789; AAA61343.1; -
DR PIR: A48077; A48077.
DR HSP: P06876; 1MBG.
DR TRAFAC: T01245; -
DR InterPro: IPR001005; MYB_DNA_binding.
DR Pfam: PF00249; myb_DNA_binding; 3.
DR SMART: SM00395; SANT; 4.
DR PROSITE: PS00337; MYB_1; 2.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS00090; MYB_3; 2.
DR Nuclear protein: DNA-binding; Transcription regulation; Repeat;
DR Phosphorylation.
DR DNA_BIND 337 382 MYB 1.
DR DNA_BIND 385 490 MYB 2.
DR SEQUENCE 595 AA; 68050 MW; 6A85334CB3AF0162 CRC64;

Query Match
Best Local Similarity 10.0%; Score 83.5; DB 1; Length 595;
Matches 28; Conservative 24; Mismatches 51; Indels 9; Gaps 2;

QY 44 PTEWNVNWNISDLKIEDLQSHMIDATLYESVHPSCVATAMKCFLELQVLSLSCG 103
DB 183 PKKXSEKSEKSGYDLNIDHDVDSVSGSLPSQVRIKRTAEVLP-----KVLSSSH 234
QY 104 DASHTDVENLITLANNLSNGN-VYESGCKECEELEKKEKPEFLOSEVHT 154
DB 235 NDDQDDVSNLIDFAAKASHIINPATQSNCKSPDESEPEALDEGFIKEYQKI 286

RESULT 12
TRZA_RHOCO
ID TRZA_RHOCO STANDARD; PRT; 476 AA.
AC 052725;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE S-triazine hydrolase (EC 3.8.1.-) (N-ethylammelane chlorohydrolase).
GN TRZA.
OS Rhodococcus corallinus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Gordoniaceae; Gordonia.
OX NCBI_TaxID=36822;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC STRAIN=NRRL 15444R;
RA MEDLINE=96011356; PubMed=7592318;
RA Shao Z.-Q., Seifens W., Mulbry W., Bekki R.M.;
RT "Cloning and expression of the s-triazine hydrolase gene (trza) from
RT Rhodococcus corallinus and development of Rhodococcus recombinant
RT strains capable of dealkylating and dechlorinating the herbicide
RT atrazine."
RL J. Bacteriol. 177:5748-5755(1995).
CC -1- FUNCTION: HYDROLYTIC DEAMINATION OF THE S-TRIAZINE SUBSTRATE
CC MELANINE.
CC -1- SIMILARITY: BELONGS TO THE ATZ/TRZ FAMILY.
CC -1- PATHWAY: Melanine degradation pathway; first step.
CC -----
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CC -----
DR EMBL: L16534; AAA90931.1; -
DR InterPro: IPR002604; ATZ_TRZ.
DR Pfam: PF01685; ATZ_TRZ; 1.
DR Hydrolase.
DR INT. MET 0 0
DR SEQUENCE 476 AA; 50727 MW; 64D953DBE92C73E CRC64;

Query Match
Best Local Similarity 9.9%; Score 82.5; DB 1; Length 476;
Matches 26; Conservative 22; Mismatches 41; Indels 21; Gaps 3;

QY 40 SAGLEPTEANW---VNVISDLKIEDLQSHMIDATLYESVHPSCVATAMKCFLELQ 96
DB 320 TVGIGTFDANQNDVSNLISDKVIALHRAHHRDASITPEKRIEMATIDGARCIGMADQ 379
QY 97 VLSLESGDAS-----LHDTVENLILAN-----NSLSSNGN 128
DB 380 ISLEAGKRADITLDRHQAQTTPAHDLAATVFOAYGENVDVLYNGSV 429

RESULT 13
TRPA_BUCSC
ID TRPA_BUCSC STANDARD; PRT; 269 AA.
AC 044604;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE tryptophan synthase alpha chain (EC 4.2.1.20).
GN TRPA.
OS Buchnera aphidicola (subsp. schlechterella chimensis)
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118110;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95261545; PubMed=7742976;
RA Lai C.-Y., Baumann P., Moran N.A.;
RT "Genetics of the tryptophan biosynthetic pathway of the prokaryotic
RT endosymbiont (Buchnera) of the aphid schlechterella chimensis."
CC -1- FUNCTION: THE ALPHA SUBUNIT IS RESPONSIBLE FOR THE ALDOL CLEAVAGE
CC OF INDOLACTYLOL PHOSPHATE TO INDOL AND GLYCERALDEHYDE 3-
CC PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate + H(2)O.
CC -1- PATHWAY: tryptophan biosynthesis; fifth (last) step.
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC -----
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CC -----
DR EMBL: 009185; AAA92797.1; -
DR HSP: P00929; 2MSV.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR002028; trp_synthaseA.
DR Pfam: PF00290; trp_synthA; 1.
DR Pfam: PF001535; trp_synthaseA; 1.
DR TIGRfam: TIGR00262; trpA; 1.
DR PROSITE: PS00167; TRP_SYNTHASE_ALPHA; 1.
DR tryptophan biosynthesis; lyase.
DR SEQUENCE 269 AA; 30301 MW; 7879A03A5C7A50MC CRC64;

Query Match
Best Local Similarity 9.7%; Score 81; DB 1; Length 269;
Matches 25; Conservative 23;

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Db      697 HPSILVDPQ-----LNVYTL-----NFCPIGDONLSYKNSKILTYLCKKH 738
Oy      137 EE---LEKKNIKPELQ 149
      ..| 111: 1:1
Db      739 KRPFYETKNIESFIQ 754

RESULT 15
R1N1-RAT      STANDARD;      PRT;      456 AA.
ID-R1N1-RAT
AC      P29315;
DT      01-DEC-1992 (Rel. 24, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Ribonuclease inhibitor.

```

RESULT 15			
R1_NL_RAT	STANDARD:	PRT:	456 AA.
ID	R1_NL_RAT		
AC	P29315:		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Ribonuclease inhibitor.		
GN	RhN.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid=10116;		
RN	[1]		
RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RP			
RC	TISSUE=lung;		
RC	MEDLINE=92162755; PubMed=1536887;		
RX	Kawanamoto M., Motojima K., Sasaki M., Hattori H., Goto S.;		
RT	"cDNA cloning and sequence of rat ribonuclease inhibitor, and tissue		
RT	distribution of the mRNA."		
RT	Biochim. Biophys. Acta 1129:335-338(1992).		
CC	FUNCTION: INHIBITOR OF PANCREATIC RNASE AND ANGIOGENIN. MAY ALSO		
CC	FUNCTION IN THE MODULATION OF CELLULAR ACTIVITIES.		

```

CC -I- SUBCELLULAR LOCATION: CYTOSOLASMIC.
CC -I- TISSUE SPECIFICITY: BRAIN, HEART, LUNG, LIVER, SPLEEN, TESTES AND
CC KIDNEY; HIGHEST IN THE LUNG AND LOWEST IN THE HEART.
CC -I- SIMILARITY: CONTAINS 15 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
DR EMBL: X62528; CAA44388.1; -.
DR PIR: S20397; S20397.
DR HSSP: P10775; 2BNH.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003590; LRR_RN1inh.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00560; LRR: 3.
DR SMART: SM00370; LRR: 12.
DR SMART: SM00368; LRR_R1: 1.
DR Repeat: Leucine-rich repeat.
DR KW Repeat 15 43 LRR A1.
DR FT REPEAT 15 43 LRR B1.
DR FT REPEAT 44 71 LRR A2.
DR FT REPEAT 72 100 LRR A2.
DR REPEAT 101 128 LRR B2.
DR FT REPEAT 129 157 LRR A3.
DR FT Repeat 185 LRR B3.

```

Query Match Best Local Similarity	Score 79: DB 1: 26.18; Pred. No. 6.5;	Length 456;
FT REPEAT	186	214 LRR A4.
FT REPEAT	215	212 LRR B4.
FT REPEAT	243	271 LRR A5.
FT REPEAT	272	299 LRR B5.
FT REPEAT	300	328 LRR A6.
FT REPEAT	329	356 LRR B6.
FT REPEAT	357	385 LRR A7.
FT REPEAT	386	413 LRR B7.
FT REPEAT	414	LRR A8.
SO SEQUENCE	456 AA; 49905 MW; 85185B1F09E5998 CRC64;	

us-09-855-313a-4.rsp

Page 9

Search completed: February 20, 2003, 16:29:05
Job time : 17.5 secs

1
2
3
4

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 16:27:07 : Search time 61.5 Seconds
(without alignments)
542,758 Million cell updates/sec

Title: US-09-855-313A-4
Perfect score: 833
Sequence: 1 MRISPHLRISIOCYCLCL.....NIKEFLOSPVHIVQMFINTS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeophage:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533	64.0	128	6	OBSPYO
2	257	30.9	187	13	OBSPYO
3	248	29.8	187	13	OBSPYO
4	117.5	14.1	143	13	OBSPYO
5	116.5	14.0	143	13	OBSPYO
6	116.5	14.0	143	13	OBSPYO
7	114.5	13.7	143	13	OBSPYO
8	111.5	13.4	143	13	OBSPYO
9	107.5	12.9	135	13	OBSPYO
10	99.5	11.9	162	4	OBSPYO
11	96.5	11.6	167	16	OBSPYO
12	89.5	10.7	167	16	OBSPYO
13	88.5	10.6	500	12	OBSPYO
14	88	10.6	382	16	OBSPYO
15	87.5	10.5	678	5	OBSPYO
16	87.5	10.5	497	8	OBSPYO

17	85	10.2	510	8	OBSPYO
18	85	10.2	1799	16	OBSPYO
19	84	10.1	167	2	OBSPYO
20	84	10.1	1249	10	OBSPYO
21	82.5	9.9	1249	16	OBSPYO
22	82.5	9.9	624	10	OBSPYO
23	81.5	9.8	489	15	OBSPYO
24	81.5	9.8	589	6	OBSPYO
25	81.5	9.8	871	15	OBSPYO
26	81.5	9.8	871	15	OBSPYO
27	81.5	9.8	871	15	OBSPYO
28	81.5	9.8	871	15	OBSPYO
29	81.5	9.8	871	15	OBSPYO
30	80.5	9.7	337	12	OBSPYO
31	80.5	9.7	642	5	OBSPYO
32	80.5	9.7	910	10	OBSPYO
33	80.5	9.7	922	5	OBSPYO
34	80	9.6	794	10	OBSPYO
35	80	9.6	882	15	OBSPYO
36	79.5	9.5	855	5	OBSPYO
37	79.5	9.5	855	5	OBSPYO
38	79.5	9.5	1553	10	OBSPYO
39	79	9.5	197	16	OBSPYO
40	79	9.5	308	2	OBSPYO
41	78	9.4	319	16	OBSPYO
42	78	9.4	492	5	OBSPYO
43	78	9.4	581	10	OBSPYO
44	78	9.4	646	16	OBSPYO
45	78	9.4	877	15	OBSPYO

ALIGNMENTS

OBSPYO	PRELIMINARY:	PRT:	128 AA.
AC	OBSPYO:		
DT	01-JUN-2002 (TRENBLER, 21, Created)		
DT	01-JUN-2002 (TRENBLER, 21, Last sequence update)		
DT	01-JUN-2002 (TRENBLER, 21, Last annotation update)		
DE	Interleukin 15 (Fragment).		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID:9615;		
RN	SEQUENCE FROM N.A.		
RA	Xiang Z., Byrne K.M., Michel J.;		
RT	Cytokine expression in muscle satellite cells of canine.		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF479882; AAL87133.1; -		
FT	NON_TER		
SO	SEQUENCE		

Query Match: 128 AA; 14192 MW; FC6RC2C2E1765934 CRC64;

OBSPYO	Best Local Similarity	64.0%;	Score 533;	DB 6;	Length 128;
Matches	102;	Conservative	11;	Mismatches	15;
				Indels	0;
				Gaps	0;
OBSPYO	1	MRISPHLRISIOCYCLCLINSHFLTEAGIHVETLIGCFESAGLPTKAMVNVISDLKRI	60		
DB	1	MRISPHLRISIOCYCLCLINSHFLTEAGIHVETLIGCFESAGLPTKAMVNVISDLKRI	60		
OBSPYO	61	EDLIOSMHIDATYTESDVHSCVATAMKCFLELVIVISLSSGASIHPTVENLITLIANN	120		
DB	61	DNLIQCHMTTLTYESDVHSCVATAMKCFLELVIVISLSSGASIHPTVENLITLIANN	120		
OBSPYO	121	SLSSNGV 128			
DB	121	DLSSKGI 128			

RESULT 2

Q9DEV5 ID Q9DEV5 PRELIMINARY: PRT: 187 AA.

AC Q9DEV5; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Interleukin 15.

GN IL-15

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

OX NCBI_TaxID=9031;

RN SEQUENCE FROM N.A.

RC TISSUE=SPLEEN;

RA Stephanak J.A., Kolodtsick J.E., Hu W., Sundick R.S.;

RT "Chicken Interleukin 15 precursor, allelic variant."

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF005476; AAC02253.1; "

DR InterPro: IPR003443; Interleukin_15.

DR Pfam: PF02372; IL15; 1

DR Pfam: PF02372; IL15; 1

DR SQUONCE 187 AA; 21964 MW; 470601BDF8837095 CRC64;

Query Match 30.9%; Score 257; DB 13; Length 187;

Best Local Similarity 39.9%; Pred. No. 1e-17;

Matches 69; Conservative 22; Mismatches 46; Indels 36; Gaps 9;

QY 5 KPLHSTISIOCYLCLLNSHFL---TEAGIHVFILGCSAGLPRTAN---VNVYISDL 57

DB 22 KTHVSTICLOLYQLLLNSHFFCLLNKKTGLTFPL---CAVYPKTEANCKMSDVAKDL 78

QY 58 KKLIEDLIQSMHIDATLTYESDVHP-SCKVTAMKCFLELQVLSLESGDASI---HPTVEN 113

DB 79 ELIK---TSEDDIVSLYANTYEDIEPCQEPWRCFPLEMKVILHEDCDIKKCSRKHDV--VNM 134

QY 114 LILANNSSLSNGN-----VTESGCKECEELEENIKETLOSFVHIQ 156

DB 135 IL-----KNGNARFATYQLNSTSKCKECEYEENKFTETLOSFVHIQ 179

RESULT 3

Q9W756 ID Q9W756 PRELIMINARY: PRT: 187 AA.

AC Q9W756; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE Interleukin-15 precursor (Interleukin 15 precursor).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

RN SEQUENCE FROM N.A.

RC STRAIN=SCUL; TISSUE=LIVER;

RA Burnside J., Sofer L.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RC STRAIN=SC; TISSUE=LIVER;

RA Choi K.D., Lillehoj H.S., Burnside J.;

RT "Gallus gallus mRNA for IL-15 precursor."

RL EMBL: AF152927; AAC8392.1; "

DR EMBL: AF152927; AAC8392.1; "

DR InterPro: IPR003443; Interleukin_15.

DR Pfam: PF02372; IL15; 1

DR SQUONCE 187 AA; 21964 MW; 470601BDF8837095 CRC64;

Query Match 29.8%; Score 248; DB 13; Length 187;

Best Local Similarity 38.5%; Pred. No. 7.9e-17;

Matches 67; Conservative 23; Mismatches 46; Indels 38; Gaps 9;

QY 5 KPLHSTISIOCYLCLLNSHFL---TEAGIHVFILGCSAGLPRTAN---VNVYISDL 57

DB 22 KTHVSTICLOLYQLLLNSHFFCLLNKKTGLTFPL---CAVYPKTEANCKMSDVAKDL 78

QY 58 KKLIEDLIQSMHIDATLTYESDVHP-SCKVTAMKCFLELQVLSLESGD---ASIDPVE 112

DB 79 ELIK---TSEDDIVSLYANTYEDIEPCQEPWRCFPLEMKVILHEDCDIKKCSRKHDV-- 132

QY 113 NLILANNSSLSNGN-----VTESGCKECEELEENIKETLOSFVHIQ 156

DB 133 -----RNKNGNARFATYQLNSTSKCKECEYEENKFTETLOSFVHIQ 179

RESULT 4

Q9PT81 ID Q9PT81 PRELIMINARY: PRT: 143 AA.

AC Q9PT81; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE Interleukin-2 precursor.

GN IL2

OS Melagris gallopavo (Common turkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.

OC NCBI_TaxID=9103;

RN SEQUENCE FROM N.A.

RC MEDLINE=20177011; PubMed=10714551;

RA Lawson S.A., Rothwell L., Kaiser P.;

RT "Turkey and chicken interleukin-2 cross-react in vitro

RL J. proliferation assays despite limited amino acid sequence identity."

DR EMBL: AF007463; CAB65230.1; "

DR InterPro: IPR000779; Interleukin-2.

DR InterPro: IPR003443; Interleukin_15.

DR Pfam: PF02372; IL15; 1

DR SMART: SM00189; IL2; 1.

KW Signal.

FT SIGNAL 1 20

FT CHAIN 21 143 INTERLEUKIN-2.

SQ SEQUENCE 143 AA; 16511 MW; 1A5DE8E7D495CCB CRC64;

Query Match 14.1%; Score 117.5; DB 13; Length 143;

Best Local Similarity 25.4%; Pred. No. 0.00056;

Matches 35; Conservative 29; Mismatches 57; Indels 17; Gaps 5;

QY 33 VFILGFSAGLKEPTEANMVN-----VISDLKIEDLIQSMHIDATLTYESDVHP 81

DB 5 VLIPSCISVALMTTAAVAGASISPEKLELLPALIKDLLEESKNKIHV--VLYTPNFI-K 61

QY 82 SCKVTAMKCFLELQVLSLESGD-ASIDPVENLILANNSSLSNGNVTESG--CKECE 138

DB 62 ECSQOTLQCYLEEMVLMKLEDEPELKNFKNALONIKRHLRLDLSPGGCKICEA 121

QY 139 LEEKNIKEPLOSFVHIQ 156

DB 122 NDKKNFPDLOQLTNFVR 139

RESULT 5

Q9IAC7 ID Q9IAC7 PRELIMINARY: PRT: 143 AA.

AC Q9IAC7; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE Interleukin-2.

GN Melagris gallopavo (Common turkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.


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DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin-2.
GN IL-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OBES;
RA Sundick R.S., G11-Dixon C.;
RT "A cloned chicken lymphokine homologous to both mammalian IL-2 and IL-
RT 15."
RL J. Immunol. 0:0-0(1997).
DR EMBL: AF000631; AAB63150.1;
DR InterPro: IPR000779; Interleukin-2.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
DR SMART: SM00189; IL2; 1.
SQ SEQUENCE 143 AA; 16307 MW; B9B1E997A54935F CRC64;

Query Match
Best Local Similarity 25.4%; Pred. No. 0.0022; Length 143;
Matches 36; Conservative 26; Mismatches 55; Indels 25; Gaps 6;

QY 33 VILGCGAGLPTTEANWVN-----VISDKRIEDLIQSMHIDATLYTESDHP 81
DB 5 VILFCISVATMTAVGASLSASAKRKLQTLKLEILENKIKHLE-LVPTPEIQ- 61
QY 82 SCVATAMKCFLELVISLSDASTHDT-VEVILLIANNSSSN-----GVNTSGCK 134
DB 62 ECTQCTLCYGEVYVTLKKTED---DTEIKEREVTAIONIEKMLKSLGNHTSGECK 117
QY 135 ECELEEKNIKEPLOSFHVQ 156
DB 118 ICEANKKKFPDFLHETNFVR 139

RESULT 9
Q9DDN9 PRELIMINARY: PRT: 135 AA.
AC Q9DDN9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Interleukin-2 (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OC NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Hu W., Kolostick J.E., Stepaniak J.A., Sundick R.S.;
RT "Turkey interleukin-2," the EMBL/Genbank/DBJ databases.
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF308569; AAG35189.1;
DR InterPro: IPR000779; Interleukin-2.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
DR SMART: SM00189; IL2; 1.
DR NON-TER 1.
SQ SEQUENCE 135 AA; 15460 MW; 326F88A3563D13E8 CRC64;

Query Match
Best Local Similarity 12.9%; Score 107.5; DB 13; Length 135;
Matches 32; Conservative 30; Mismatches 54; Indels 17; Gaps 5;

QY 38 CFSAGLPTTEANWVN-----VISDKRIEDLIQSMHIDATLYTESDVHPSCKVT 86

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DB 2 CISVALMTAVGASLSPEKLEIPALIKDLEHLESKKIIV--VLTPENI-KKCSQO 58
QY 87 AMKCFLELVISLSDG-ASIHDTVENILLIANNSSNGVNTSG--CKEELELEEN 143
DB 59 TLQCTLEEMVWLELEDEDEPEIKNEFNALQNIKNLHRLKGLSPTGGECKICEANDKN 118
QY 144 IKEFLOSFHVQ 156
DB 119 FPDFLOQLNLR 131

RESULT 10
Q9HBE4 PRELIMINARY: PRT: 162 AA.
AC Q9HBE4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 21.
GN IL21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20531754; PubMed=11081504;
RA Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burhead S., Heipel M., Brandt C., Kulper J.L., Kramer J.,
RA Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamby K.,
RA Mudd S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Rayner F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kausansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and
RT regulation of lymphocyte function."
RL Nature 408:57-63(2000).
DR EMBL: AF254069; AAC29348.1;
SQ SEQUENCE 162 AA; 18652 MW; 54EPD4ED3AB97FE CRC64;

Query Match
Best Local Similarity 25.9%; Pred. No. 0.04; Length 162;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY 51 VNVISDURK-IEDLIQSMHIDATLYTESDVHPSCKVATAMKCFLELVISLSDGASIH 109
DB 43 IDIVDQKMYNDLVPEF---LPAPEVETKEMSAPSC---QKQKLSANNGNE 93
QY 110 TVENLIT--IANNSSNGVNTSG--CKEELEEKNIKEPLOSFHVQMPIN 160
DB 94 KIIVSIRKLKRRKPRSTINACRQKRLTCTPSDYEKKPKPELFKFSLLQMKIH 149

RESULT 11
Q9ZGE7 PRELIMINARY: PRT: 433 AA.
AC Q9ZGE7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical protein R01176.
GN R01176.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OC NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAISH 7;
RA MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renseto-Audiffren P., Fournier P.-E., Barde V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;

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RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii".
 RL Science 293:2093-2098(2001).
 DR EMBL: AF008665; AL03714.1; -
 KW Hypothetical protein; Complete proteome.
 SO SOURCE 433 AA; 48342 MW; 4934702460B02EE6 CRC64;

Query Match 11.6%; Score 96.5; DB 16; Length 433;
 Best Local Similarity 19.7%; Pred. No. 0.27;
 Matches 37; Conservative 38; Mismatches 66; Indels 47; Gaps 8;

QY 10 SISQCYCLLN-----SHFLTEAGIHVF-----ILCCFSAQ--LPKTEAMV 51
 DB 6 NINRCWPIFSNVEIVSRISQVSHIHKLSSTFSSVSTVEGARFKGYTDNTQCMWK 65
 QY 52 NVISDLKIEDLIQSMHIDA-----TYESDVHPSCKVTAKCFLELOVLSIES 102
 DB 6 NFEQFESHPNFSIHQECNNGINPINNITFDENPH-----ILLQOVTTPHON 117
 QY 103 GDASHDTEVENIILANSSLSNGVTESS-----GKCEEELEFNKEFLOSVHIV- 155
 DB 118 GTASI---LSQYKYMNDYFESQGNITETSGADFLGNETCKREANMIALONNATYETLI 174
 QY 156 --QMFTNT 161
 DB 175 PRESENT 182

RESULT 12

08XPC3 PRELIMINARY: PRT: 167 AA.
 AC 08XPC3;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 GN CP00042.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
 RA "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL: AP003185; BAB79748.1;
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 167 AA; 18821 MW; AD25C7DC5765B3A CRC64;

Query Match 10.7%; Score 89; DB 16; Length 167;
 Best Local Similarity 21.9%; Pred. No. 0.46;
 Matches 32; Conservative 28; Mismatches 50; Indels 36; Gaps 4;

QY 31 IHVFLICFSAGLPKTEAMVNVISD-----LKKIEDLIQSMHIDATLYTE 76
 DB 14 ISLVLCSTSTG---EKNTINIPLEKSRDEEEDYDTSTSTVMSVDSIKNM 69
 QY 77 SDVHPSCKV-----TAKCFLELOVLSIESGDASHDTEVENIILANSSLS 124
 DB 70 RTVSENGKLNINMIDLRSNNEFKCLIEDLGKGVVPEKFSYVNDIINNKKATSTSEA 129
 QY 125 NGVNTSGKCEEELEFNKEFLOSVHIV- 155
 DB 130 MKNSHD-----EFTKSNKIFVES 149

RESULT 13
 09YWB5 PRELIMINARY: PRT: 500 AA.
 ID 09YWB5

AC 09YWB5;

DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE ORF MSY008 leucine rich repeat gene family protein, similar to Amsacta
 DE moorei entomopoxvirus Q3 ORF SW:P28854.
 GN MSY008
 OS Melanoplus sanguinipes entomopoxvirus (MSFPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
 OC Entomopoxvirus B.
 OX NCBI_TaxID=83191;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RX MEDLINE=99102612; PubMed=9847359;
 RA Afonso C.L., Tujman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.,
 RT "The genome of Melanoplus sanguinipes entomopoxvirus".
 RL J. Virol. 73:533-552(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RA Afonso C.L., Tujman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.,
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases
 DR EMBL: AF063866; AAC97859.1;
 SO SEQUENCE 500 AA; 58567 MW; 75DC7F13BBFBCA9 CRC64;

Query Match 10.6%; Score 88.5; DB 12; Length 500;
 Best Local Similarity 21.8%; Pred. No. 2;
 Matches 49; Conservative 43; Mismatches 60; Indels 73; Gaps 12;

QY 3 ISKPLRST--SISQCYCLLNSHFLTEAGIHVFILG-----C-FSAGLPKTEA 48
 DB 90 IYKCKLSLKLKLNCKECKIIDFKFL-ESLINLEILDISYKNSNIYKCKLSLKLKNC 148
 QY 49 MWVVISDLKIEDLIQSMHIDATLYTESDVHP-----SCVTFMKCF--LL 93
 DB 149 NECKLI-DFKFLPSLNLNLEILDVYKNSNIYECTPLSLLELKCSKIIDFKFLSLI 207
 QY 94 ELOVISLESQDS-----IHD-----YVENIILANSSLSNGV 128
 DB 208 NLEILDVSNESNISDCKLPVSLIKLNCERCYIYDKFLEPLNKKIL-NISYKNSNI 266
 QY 129 TSGCKCEEELEFNKEFLOSVHIVQMFINTS 162
 DB 267 S-----DCKLPVSLIKLNCYCYIYDKFLEPLNKKILNLSN 306

RESULT 14

08XNB9 PRELIMINARY: PRT: 382 AA.
 AC 08XNB9;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 GN Alcohol dehydrogenase.
 OR ADH OR CP00449.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
 RA "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL: AP003186; BAB80155.1;
 DR InterPro: IPR001670; Fe-ADH.
 DR Pfam: PF00465; Fe-ADH; 1.
 DR PROSITE: PS00913; ADH_IRON_1; 1.

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DR PROSITE: PS00060; ADH_IRON_2; 1.
KW Complete proteome.
SQ SEQUENCE 382 AA; 40823 MW; 80300D0269F22E32 CRC64;

Query Match
Best Local Similarity 31.4%; Pred. No. 1.6; 44; Indels 8; Gaps 5;
Matches 33; Conservative 20; Mismatches 17; Last annotation update)

OY 20 LNSHTFTEAGIHVEITIGCSAGLPTEANWVNSDLKIEDLIOSMHDATLYTESDV 79
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 LMGADCLKADGQVGEELG-FKKALIVTD-KVLGOIGYKKVTVDLNDKNIEAYIDETFP 69
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 80 HPSCK-VTAMKCFLELD---VISTESGDASITDVTENLIILANN 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 70 NPTVKVNDGLALKEKECFVISTL--GGGSAMDCAKGIALLATN 112
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ID 061493 PRELIMINARY; PRT; 678 AA.
AC 061493.
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Hook protein.
DE Hook OR HK.
OS Drosophila virilis (fruit fly). Tracheata; Hexapoda; Insecta;
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID-7244;
RN [1]
RP Phistery M., Sunio A., Kramer H.;
RA Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF044926; AAC09301.1; -;
DR FlyBase: FBgn0024376; Dvir\hook.
SQ SEQUENCE 678 AA; 77198 MW; 1B8535E80F06C673 CRC64;

Query Match
Best Local Similarity 23.3%; Pred. No. 3.2; 46; Indels 50; Gaps 6;
Matches 37; Conservative 26; Mismatches 11;

OY 49 NNVNVIISDLKIEDLIOSMHDATLYT--ESDVHPSCKVTAACFLELDV----- 98
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 NNRLEMSNLKVEGYEYSDVLTLOHDFVKPDVQALAEKCDLSELRLOLYLGA 123
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 99 -----SIESGDASITDVTENLIIL--LANNSS--NGNV 128
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 VNCARKOSYICELMCEELQANIRALQELLESSTRTQTEGGVSSLSRNSLSGMLDGA 183
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 129 -----TESGCKECELEKNI-----KEFLQSFVHYOM 157
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 KALEERDAMAKCFETEEKMLLLIDCKTNLOQELHKLQL 222
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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